

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2000, 12:32:43 ; Search time 1178.81 Seconds
(without alignments)
6086.469 Million cell updates/sec

Title: US-09-142-471-1
Perfect score: 1627
Sequence: 1 gtcacgcagtgagtgtag.....gtacgatgggcacccgtgac 1627

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*

44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: em_est35:*
83: em_est36:*
84: em_est37:*
85: gb_est48:*
86: gb_est49:*
87: gb_est50:*
88: gb_est51:*
89: gb_est52:*
90: gb_est53:*
91: gb_est54:*
92: gb_est55:*
93: gb_gss1:*
94: gb_gss2:*
95: gb_gss3:*
96: gb_gss4:*
97: em_gss1:*
98: em_gss2:*
99: em_gss3:*
100: em_gss4:*
101: gb_gss5:*
102: gb_gss6:*
103: gb_gss7:*
104: gb_gss8:*
105: gb_gss9:*
106: em_gss5:*
107: em_gss6:*
108: em_gss7:*
109: em_gss8:*
110: em_gss9:*
111: em_gss10:*
112: em_gss11:*
113: gb_gss10:*
114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*

117: gb_gss13:*
 118: gb_gss14:*
 119: gb_gss15:*
 120: gb_gss16:*
 121: gb_gss17:*
 122: gb_gss18:*
 123: gb_gss19:*
 124: em_gss13:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	380	23.4	517	79	AW630744	W630744 hh87a03.y
2	372.2	22.9	595	91	W31016	W31016 zb85e08.r1
3	364	22.4	481	43	AI751501	AI751501 cn10cl2.y
C 4	297.4	18.3	771	43	AI735329	AI735329 at09c06.x
C 5	286.4	17.6	731	35	AI085963	AI085963 o286h01.x
C 6	281	17.3	725	44	AI824041	AI824041 wj29h07.x
7	248.6	15.3	287	89	T29234	T29234 EST73852.Hu
C 8	240.2	14.8	655	40	AI472218	AI472218 t186e02.x
9	216.4	13.3	280	25	AA381568	AA381568 EST94686
10	210	12.9	618	91	W51812	W51812 zc48h04.r1
11	186	11.4	311	25	AA381892	AA381892 EST95205
12	172.4	10.6	316	25	AA380919	AA380919 EST93950
C 13	169.2	10.4	594	38	AI343270	AI343270 tb94c07.x
14	148.2	9.1	311	79	AW630409	AW630409 hh76g07.y
15	139	8.5	628	47	AI982185	AI982185 pat_pk007
16	128	7.9	170	25	AA362308	AA362308 EST71834
C 17	125.6	7.7	463	43	AI751500	AI751500 cn10cl2.x
C 18	106.2	6.5	525	33	AA947476	AA947476 ok20h06.s
19	95.6	5.9	498	28	AA553279	AA553279 vk82h10.s
C 20	91.2	5.6	562	30	AA721478	AA721478 nz74g01.s
C 21	81	5.0	636	69	AW214008	AW214008 uo46e09.x
C 22	79.2	4.9	657	121	B87803	B87803 RPC111-30H2
C 23	77	4.7	601	73	AW519504	AW519504 up33e08.y
C 24	76.6	4.7	416	94	AQ135450	AQ135450 HS_3053.A
25	74	4.5	196	25	AA381453	AA381453 EST94531
26	70.2	4.3	617	79	AW637075	AW637075 bl54a09.w
C 27	65.8	4.0	493	35	AI095255	AI095255 ov18h07.s
C 28	58.4	3.6	925	122	CNS0091P	AL053013 Drosophil
C 29	53.2	3.3	473	35	AI074123	AI074123 o254c06.x
C 30	53	3.3	441	73	AW503691	AW503691 UI-HF-BN0
31	52.6	3.2	925	122	CNS0091P	AL053013 Drosophil
32	51.2	3.1	385	72	AW437358	AW437358 78370 MAR
C 33	51.2	3.1	464	69	AW243012	AW243012 xn28c05.x
34	50.2	3.1	839	122	CNS004NB	AL054280 Drosophil
C 35	49	3.0	645	122	CNS01213	AL101589 Drosophil
C 36	47.6	2.9	932	122	CNS0072Q	AL066742 Drosophil
37	47.2	2.9	935	122	CNS006KK	AL066051 Drosophil
C 38	47	2.9	1101	123	CNS017SY	AL108460 Drosophil
39	46.8	2.9	932	122	CNS0072Q	AL066742 Drosophil
C 40	46.2	2.8	477	64	AW134706	AW134706 UI-H-B11-
C 41	46.2	2.8	477	64	AW134707	AW134707 UI-H-B11-
C 42	45.6	2.8	361	89	T28073	T28073 EST26562.Hu
43	44	2.7	446	27	AA495728	AA495728 zw04a09.i
44	43.6	2.7	910	122	CNS006ON	AL065629 Drosophil
C 45	43.2	2.7	776	122	CNS010RY	AL099352 Drosophil

ALIGNMENTS

RESULT 1
 AW630744
 LOCUS
 DEFINITION hh87a03.y1 NCI-GAP.GUI Homo sapiens cDNA clone IMAGE:2969740 5' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA
 EST 31-MAR-2000

sequence.
 AW630744
 VERSION
 AW630744.1 GI:7377534
 EST.
 KEYWORDS
 SOURCE
 HOMO SAPIENS

REFERENCE
 1 (bases 1 to 517)
 NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished (1997)
 On Jan 6, 2000 this sequence version replaced gi:6676648.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
 Seq primer: -40RP from Gibco
 High quality sequence stop: 422.

FEATURES
 Location/Qualifiers
 1..517
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2969740"
 /clone_lib="NCI-GAP.GUI"
 /tissue_type="2 pooled high-grade transitional cell tumors"
 /lab_host="DH10B"
 /note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."
 BASE COUNT 149 a 139 c 123 g 106 t
 ORIGIN

Query Match 23.4%; Score 380; DB 79; Length 517;
 Best Local Similarity 98.7%; Pred. No. 8.4e-89;
 Matches 383; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1057 ccagttacccccaggagaagattccaaagattagcgcgcacacagacagcactcacc 1116
 Db 130 CCAGTACCCCGAGGAGAAGATTCCAAAGATGTAGCGCGCCACACAGACAGCCTCACC 189
 Qy 1117 tcttcagaaacaaattgacaaacaaattcggtacatcctcgagcgcatctcagccctgaga 1176
 Db 190 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCTCGAGCGCATCTCAGCCCTGAGA 249
 Qy 1177 aaggagacatgtacaagagtaacatgtgtgaaacagacaaagagcactgagcagaaaaac 1236
 Db 250 AAGGAGACATGTAAACAGAGTAACATGTGTGAAGCAGCAAGAGGCGACTGCGCAGAAAAC 309
 Qy 1237 aacctgaacctccaaagatggctgaaagagatgattcctccaatctggattcaatgag 1296
 Db 310 AACCTGAACCTTCCAAAGATGCTGAAAAGATGATGATCTTCCAATCTGGATTCAATGAG 369
 Qy 1297 gagactgctgggtgaaacatcatcactggtcttttggatttgaggtatcactagtagtac 1356
 Db 370 GAGACTTGGTGGTGAATATCATCTGCTCTTTTGGAGTTTGGAGTATACCTAGAGTAC 429
 Qy 1357 ctccagacagatttgagtagtgaggagaaacagccagagctgtgcagatgagtacaaaa 1416
 Db 430 CTCCAGAACAGATTGACAGTAGTGAGGACCAAGCCAGAGCTGTGCACATGAGTACAAA 489
 Qy 1417 gtctgtatccagttctcctgcagaaaaagg 1444

Qy	1177	aaggagacatgtaacaagaagttaacctgtgtgtgaagcagcaagaaggccactgcgcgaaaac	1235
Db	264	AAGGACACATGTAAACAAGAGTAACTAATGTGTGAAGCAGCAAGAAGAGGCACACTGGCGAAAAAC	323
Qy	1237	aacctaaaccttccaagattggct-gaaaaagatggatgctttccaatctggattaccaatga	1295
Db	324	AACTGAACCTCCCAAAGATGGCTGAAAGAAATGGATGCTTCCAANTGGATTCAATGA	383
Qy	1296	ggagacttgctgtgtaaatacatcac-tgggtcttttgagtttgaggtatcacctagagt	1354
Db	384	GGAGACTTGCTTGGTGAANAATCATCACITGGTCCTTTTGAGGTTTGAGGTATACCTAGAGT	443
Qy	1355	acctccagAACAGATTTGAGAGTAGTTGAGGAACAAAGCCAGAGCTGTGCAGATGAGTACA	1413
Db	444	ACCTCCAGAACAGATTTGAGAGTAGTTGAGGAACAAAGCCAGAGCTGTGCAGATGAGTACA	503
Qy	1414	aaagtctgatccagtctctcgagaaaaggcaagaatatctagatgcaataaccacccc-	1472
Db	504	AAGTCTGTATCCAGTTCCTTTGCAGAAAAAGGCCNAAGAAATCTAGATGCNATNACCACCCCT	563
Qy	1473	tgaccacacccccaatgccagctcgtcgacga	1504
Db	564	TGACCCCCAACCAATGGCCAGCCTGCTGACGA	595
RESULT 3			
AI751501			
LOCUS			
DEFINITION			
AI751501.1 Normal Human Trabecular Bone Cells Homo sapiens cDNA			
clone NHTBC_cn10c12 random, mRNA sequence.			
AI751501			
AI751501.1 GI:5129765			
EST.			
SOURCE			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS			
Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M., Robey,P.G., Hotchkiss,R.N. and Franccomano,C.A.			
SGAP: The Skeletal Genome Anatomy Project			
Unpublished (1997)			
TITLE			
JOURNAL			
COMMENT			
On Jun 22, 1998 this sequence version replaced gi:3247051.			
Contact: Libin Jia			
Medical Genetics Branch			
National Human Genome Research Institute			
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA			
Tel: 301-402-4877			
Fax: 301-496-7157			
Email: libin@helix.nih.gov			
DNA Sequencing and analyses by National Institutes of Health			
Intramural Sequencing Center (NISC).			
Plate: 10 row: c column: 12			
Seq primer: M13RP1 reverse primer (ABI).			
Location/Qualifiers			
1..481			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/clone="NHTBC_cn10c12"			
/clone_lib="Normal Human Trabecular Bone Cells"			
/sex="Female"			
/tissue_type="Bone"			
/cell_type="Trabecular Bone Cells"			
/lab_host="SURE"			
/note="Organ: Hip; Vector: pBluescript; Site_1: EcoR1"			
BASE COUNT 137 a 131 c 112 g 101 t			
ORIGIN			
Query Match 22.4%; Score 364; DB 43; Length 481;			
Best Local Similarity 100.0%; Pred. No. 1.3e-84;			
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps			

Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghegan, N.S.M., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinklejr, P.S., Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)

JOURNAL
MEDLINE
COMMENT

On Dec 20, 1995 this sequence version replaced gi:1135864.

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 301869056

Fax: 301869423

Email: tdbinfo@db.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).

Insert Length: 716 Std Error: 0.00

Seq primer: M13 Reverse

High quality sequence stop: 92.

Location/Qualifiers

FEATURES

source

1..287

/organism="Homo sapiens"

/db_xref="ATCC (inhost):105671"

/db_xref="taxon:9606"

/clone.lib="Human Bone"

/tissue.type="bone"

BASE COUNT 81 a 69 c 68 g 65 t 4 others

ORIGIN

Query Match 15.3%; Score 248.6; DB 89; Length 287;

Best Local Similarity 96.9%; Pred. NO. 1.6e-54;

Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1368 atttaagatgtaggacaagccagagctgtgcagatgatacaaaagtcctgatacca 1427

Db 1 ATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGATACAAANTCCTGATCCA 60

QY 1428 gtctctgcagaaaaggcaagaattctagatgcaataaccacccctgaccccaaccacaaa 1487

Db 61 NTCTCTGCAGAAAGGCAAGANTCTAGATGCAATAACCACCCCTGACCCAAACACAAA 120

QY 1488 tgcagcctctgtacgaagctgcaggaacagaccagtgctgcaggagacatacactca 1547

Db 121 TGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGACATGACAACCTCA 180

QY 1548 tctcattctgcagctttaagagattctctcagtcacagctgagggctcttcggcaaat 1607

Db 181 TCTCAATTCGCGAGTTTTAAGAGTTCTCTGCAGTCCAGCCCTGAGGGCTCTTCGGCAAT 240

QY 1608 gtacgatggcaccgtcga 1626

Db 241 GTAGCATGGCACCCTCAGA 259

RESULT 8

AI472218/c

LOCUS

DEFINITION

tj86e02.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone

IMAGE:2148410 3' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR

(HUMAN); mRNA sequence.

14-APR-1999

EST

655 bp

mrna

AI472218

Soares NSF_F8_9W_OT_PA_P_S1

Homo sapiens

cDNA clone

IMAGE:2148410 3'

similar to gb:X04430

INTERLEUKIN-6

PRECURSOR

(HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

human sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 655)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On May 18, 1998 this sequence version replaced gi:3138589.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 709 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 444.

Location/Qualifiers

1..655

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="Soares NSF_F8_9W_OT_PA_P_S1"

/lab.host="DH10B"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not 1; Site_2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was

PCR-amplified cDNAs from pools of 5,000 clones made from

the same 5 libraries. The pools consisted of the following

libraries and clones: Soares NBHSF pool 1:

309384-310919, 323208-325895 Soares NB2HP pool 1:

145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares NB2HP-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NBHPA

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 201 a 125 c 113 g 213 t 3 others

ORIGIN

Query Match 14.8%; Score 240.2; DB 40; Length 655;

Best Local Similarity 97.6%; Pred. No. 3e-52;

Matches 242; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1379 ctgaggaacagccagagctgtgcagatgatacaaaagctcaggttcctgcaga 1438

Db 655 GTGAGGANCAGCCAGAGCTGTGCAGATGATGACAAAAGTCNTGATCCAGTCTCCGAGA 596

QY 1439 aaaaagcaaaagaattagatgcaataaccacccctgaccccaaccacaaatgccagcctgc 1498

Db 595 AAAAGGCAAGAATCTAGATGCAATAACCACCCCTGACCCCAACCAATGCCAGCCTGC 536

QY 1499 tgaagaagctgcaggacagacaccagtggtgcaggagacatgacaactcatcttcgc 1558

Db 535 TCACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGACATGACAACTCATCTCATTCGCG 476

QY 1559 gcagctttaagagattcctgcagtcacagccttcgagggcttcgcaaatgtagatgggc 1618

Db 475 GCAGCTTTAAGAGATTCTCTGCAGTCCAGCTCCAGGCTTCTTCGGCAATGATGATGGGC 416

QY 1619 accgtcga 1626

Db 415 ACCTCAGA 408

[illegible]

```

Qy 1467 caccctgacccaaaccacaaatgccagcctgctgacgaagctgcaggccacagaacacgtg 1526
|||||
Db 73 CACCCTGACCCAAACCAAAATGCCAGCTGCTGACGAAGCTGCAGGACACAGAACCACTG 132

Qy 1527 gctcagagacatgacaactcatctctctcgtcgcagcgttttaaggagttcctcgcagtcacg 1586
|||||
Db 133 GCTCAGAGACATGACAACATCATCTCATCTCGCGCAATTTTAAGGAGTTCCTCGAGTCCAG 192

Qy 1587 cctgaggctcttcggcaaatgtagcagggcaccgctcga 1626
|||||
Db 193 CTTGAGGCTCTTCGGCAAAATGATCATCGGACACCTCAGA 232

RESULT 11
AA381892 311 bp mRNA EST 21-APR-1997
LOCUS AA381892
DEFINITION EST95205 Activated T-cells 1 Homo sapiens cDNA 5' end similar to
interleukin 6, mRNA sequence.
ACCESSION AA381892
VERSION AA381892.1 GI:2034376
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
12140200
Other_ESTs: THC167228
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M3 Reverse.
Location/Qualifiers
1. .311
/organism="Homo sapiens"
/db_xref="ATCC (inhost):186438"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells I"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 86 a 99 c 68 g 58 t
ORIGIN

```

```

Query Match 11.4%; Score 186; DB 25; Length 311;
Best Local Similarity 100.0%; Pred. No. 3.6e-38;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1057 ccagtacccccaggagagattccaaaagttagtcgccccacacagacagccactcacc 1116
|||||
Db 126 CCAGTACCCCGGAGAGATTCCAAAGATGTAGCGCGCCACACAGACAGCCACTCACC 185

Qy 1117 tcttcagacaaattgacaaaatttcggtacattcctcgcagcgcattcgcacctgaga 1176
|||||
Db 186 TCTTCAGAACGAATTGACAAACAATTCGGTACATCTCGAGCGGATCTCAGCCCTGAGA 245

Qy 1177 aaggagacatgtaacaagtagtaacatgtgtgaacagcagaagcgcactgcgcaaaaac 1236
|||||
Db 246 AAGGAGACATGTAAACAGATTAACATGTGTGAACAGCAGAAAGAGGCACTGGCAGAAAAC 305

Qy 1237 aacctg 1242
|||||
Db 306 AACCTG 311

RESULT 12
AA380919 316 bp mRNA EST 21-APR-1997
LOCUS AA380919
DEFINITION EST93950 Activated T-cells V Homo sapiens cDNA 5' end similar to
interleukin 6, mRNA sequence.
ACCESSION AA380919
VERSION AA380919.1 GI:2033259
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
12140200
Other_ESTs: THC167228
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M3 Reverse.
Location/Qualifiers
1. .316
/organism="Homo sapiens"
/db_xref="ATCC (inhost):185336"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells V"

FEATURES
source

```

```

/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      82 a 103 c 72 g 58 t 1 others
ORIGIN

Query Match      10.6%; Score 172.4; DB 25; Length 316;
Best Local Similarity 98.9%; Pred. No. 1.3e-34;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1057 ccagtagcccccagagaagattccaaagatgtagcgcgcacacagagccactcacc 1116
Db 142 CCAGTACCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACAGACAGCCACTCACC 201
QY 1117 tcttcgaacgaattgacaaacaaattcggtacatctctcagcgcctcagccctgaga 1176
Db 202 TCTTCAGACGAATTGACAAACAAATTCGGTACATNCTCGACGGCATCTCAGCCCTGAGA 261
QY 1177 aaggagacatgtacaagagtaacatgtgtgaagcagcagaagaggcactggcag 1231
Db 262 AAGGAGACATGTACAGAGTACATGTGTAAAGCAGCAAGAGGCCTGGCAG 316

RESULT 13
AI343270/c
LOCUS      AI343270      594 bp      mRNA      EST      18-MAR-1999
DEFINITION tb94c07.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2061996 3'
similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION  AI343270
VERSION     AI343270
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 594)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/dbrr/image/image.html
            Insert Length: 823 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 473.
FEATURES
    source
        1..594
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2061996"
            /clone_lib="NCI_CGAP_Col6"
            /tissue_type="colon tumor, RER+"
            /lab_host="DH10B"
            /note="Organ: colon; Vector: pT73B-Pac (Pharmacia) with a
            modified polylinker; Site_1: Not I; Site_2: Eco RI;
            Plasmid DNA from the normalized library NCI-CGAP.Col6 was
            prepared, and ss circles were made in vitro. Following HAP
            purification, this DNA was used as tracer in a subtractive
            hybridization reaction. The driver was PCR-amplified cDNAs
            from a pool of 5,000 clones made from the same library
            (cloneIDs 1057416-1061255, and 1144584-1145351)."

```

```

Subtraction by Bento Soares and M. Fatima Bonaldo.
BASE COUNT      197 a 109 c 100 g 188 t
ORIGIN

Query Match      10.4%; Score 169.2; DB 38; Length 594;
Best Local Similarity 97.8%; Pred. No. 1.1e-33;
Matches 182; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1442 agcacaagaatctagatgcaat-aaccacccctgaccacacacaaatgccagctgctg 1500
Db 594 AGCAAGAATCTAGATGCAATAAACCCCTGACCCCAACACCAAAATGCCAGCTGCTGTG 535
QY 1501 acgaagctgcaggcacagaacacagtcgctgcagacatgacaaactcatctctgcgc 1560
Db 534 ACGNAGTGGCAGGCACAGAACCACTGCTGCAGGACATGACAACTCATCTCTCTCGCC 475
QY 1561 agcttaagagagttcctgcagtcagtcagcgcctgagggctctcgccaaatgtagcatgggac 1620
Db 474 AGCTTTAAGGAGTTCCTGCAGTCCAGCTCAGGGCTCTTCGGCAAATGTAGCATGGGCAC 415
QY 1621 cgtcga 1626
Db 414 CTCAGA 409

RESULT 14
AW630409
LOCUS      AW630409      311 bp      mRNA      EST      31-MAR-2000
DEFINITION hh76g07.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968764 5'
similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN); contains
PTR5.b1 PTR5 repetitive element ;, mRNA sequence.
ACCESSION  AW630409
VERSION     AW630409
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 311)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            Seq primer: -40RP from Gibco
            High quality sequence stop: 213.
FEATURES
    source
        1..311
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2968764"
            /clone_lib="NCI_CGAP_GU1"
            /tissue_type="2 pooled high-grade transitional cell
            tumors"
            /lab_host="DH10B"
            /note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
            Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
            Primer: Oligo.dT. Library constructed by Life
            Technologies."
BASE COUNT      76 a 96 c 77 g 60 t 2 others
ORIGIN

```

Query Match 9.1%; Score 148.2; DB 79; Length 311;
Best Local Similarity 96.4%; Pred. No. 2.7e-28;
Matches 161; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1057 ccagtcacccccaggagaagatccaaagatgtagcgcgcacacacagacagaccactcacc 1116
|||||
DB 138 CCAGTACCCCGAGGAGAGATTCCTAAAGATGTAGCGCGCCACACAGACAGACGCACTCACC 197
|||||
QY 1117 tcttcagacgaattgacaaacaaattcgggtacattcctcgacggcatctcagccctgaga 1176
|||||
DB 198 TCTTCAGAACGAATTGACAAACAATNTCGGTACGTCCTCGACGGCATCTCAGCCCTGAGA 257
|||||
QY 1177 aaggagacatgtacaacagtaaca-tgtgtgaagcagcgaagagg 1222
|||||
DB 258 AAGGAGACATGTACANGAGTAGCATTTGTGTGAAGACGACCAAGAGG 304
|||||

RESULT 15

AI982185 628 bp mRNA EST 15-SEP-1999
LOCUS pat.pk0076.f2.f chicken activated T cell cDNA Gallus gallus cDNA
DEFINITION clone pat.pk0076.f2.f 5' similar to interleukin-6, mRNA sequence.

ACCESSION AI982185

VERSION AI982185.1 GI:5885213

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 628)

AUTHORS Tirunagaru, V.G., Sofer, L. and Burnside, J.

TITLE An expressed-sequence-tag database of activated chicken T cells:
sequence analysis of 5596 clones

JOURNAL Unpublished (1999)

COMMENT On Jun 22, 1998 this sequence version replaced gi:3247580.

Contact: Joan Burnside

Molecular Endocrinology

University of Delaware

40 Townsend Hall, Newark, DE 19717, USA

Tel: 302 831-1345

Fax: 302 831-3651

Email: joaneUdel.Edu

Seq primer: T7.

FEATURES Location/Qualifiers

source

1..628

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="pat.pk0076.f2.f"

/clone_lib="chicken activated T cell cDNA"

/sex="male"

/cell_type="Con A-activated splenic T cell"

/lab_host="E.coli TOP10 F"

/note="vector: pcDNA3"

BASE COUNT 152 a 170 c 177 g 128 t 1 others

ORIGIN

Query Match

Best Local Similarity 8.5%; Score 139; DB 47; Length 628;
Matches 262; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1144 cgggtacatctcgaggcatctcagccctgagaagaagagacatgtaacaagagtaacatg 1203
|||||

DB 45 CGGTGCTCGCGACCGCGCCCTCCAGCTGCGAGGAGAGATGTGCAAGAGTTTCCCGTG 104
|||||

QY 1204 tgtgaagcagcaagaaggcactggcagaacaaacacccctgaaccttccaaagatgggtgaa 1263
|||||

DB 105 TCGGAGAACAGCATGAGATGCTGCTCCGGAACAACCTCAACCTGCCCAAGGTGACGGAG 164
|||||

QY 1264 aaagatggaatgttccaatctggattcaatgagagagacttgctggtgaaatcatcact 1323
|||||

Db 641 gtgagtggtgctcggagcagcccccatccctgagcagcaaaagctgtgctcttggtagga 700
Qy 488 agtttcagaaacagtcgccgccaagaacttccaggagccgtgcagtgattccagagatccc 547
Db 701 agtttcagaaacagtcgccgccaagaacttccaggagccgtgcagtgattccagagatccc 760
Qy 548 agaaagttctctcgtccagtagcagtcgccggaaggagagacagctcttctacatagtgcca 607
Db 761 agaaagttctctcgtccagtagcagtcgccggaaggagagacagctcttctacatagtgcca 820
Qy 608 tctgctgcgcagtagtgctcgggagcaagttcagcaaaactcaaaccttccaggggtgtg 667
Db 821 tctgctgcgcagtagtgctcgggagcaagttcagcaaaactcaaaccttccaggggtgtg 880
Qy 668 gaatttcagcctgatccgctgcgaacatcacagtcactgcctgagcagaaaccccc 727
Db 881 gaatttcagcctgatccgctgcgaacatcacagtcactgcctgagcagaaaccccc 940
Qy 728 gctggtcagtgctacctggcaagacccccactcctggaactcatcttctacagactac 787
Db 941 gctggtcagtgctacctggcaagacccccactcctggaactcatcttctacagactac 1000
Qy 788 ggttgagctcagatagtcggctgaacggtcaaaagacattcaaacatggtgccaagg 847
Db 1001 ggttgagctcagatagtcggctgaacggtcaaaagacattcaaacatggtgccaagg 1060
Qy 848 acctccagcatcactgtgtcatccacgacgctgagcgcgtgagcgacgtggtgcagc 907
Db 1061 acctccagcatcactgtgtcatccacgacgctgagcgcgtgagcgacgtggtgcagc 1120
Qy 908 tctgtgccaggagagtgctcggcgaaggcagtgagcgagtgagcgccgagggccatgg 967
Db 1121 tctgtgccaggagagtgctcggcgaaggcagtgagcgagtgagcgccgagggccatgg 1180
Qy 968 gcacgcttgagacagaatccaggagctcctccagct 1002
Db 1181 gcacgcttgagacagaatccaggagctcctccagct 1215

RESULT 2

5480796-1

; Patent No. 5480796

; APPLICANT: KISHIMOTO, TADAMITSU

; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

; FOR HUMAN B CELL STIMULATORY FACTOR-2

; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/907,650

; FILING DATE: 02-JUL-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 298,694

; FILING DATE: 19-JAN-1989

; SEQ ID NO:1:

; LENGTH: 2061

5480796-1

Query Match

Best Local Similarity 61.2%; Score 995; DB 7; Length 2061;

Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 catgagtggtgagcagagaggaagcatgctggccgtgcgtgcgtgcgtgcgtgcgtgc 67
Db 221 catgagtggtgagcagagaggaagcatgctggccgtgcgtgcgtgcgtgcgtgc 280
Qy 68 tctgtgc 127
Db 281 tctgtgc 340
Qy 128 gaggcgctgaccagctgcgcagagacagcgtagctgacctgacctgccccgggtagagc 187
Db 341 gaggcgctgaccagctgcgcagagacagcgtagctgacctgacctgccccgggtagagc 400

QY	394	tgcttcggaagcggccctcagcaatgtgttggtagtgggtctctcgaggaccacca	453		Db	61	gccccaggcgctgcctgcgaggaggtggcaagagcgctgctgcaccagctctgcacgga	120	
Db	361	tgcttcggaagcggccctcagcaatgtgttggtagtgggtctctcgaggaccacca	420		QY	154	gacagcgtgactctgactctgactctgactctgactctgactctgactctgactctg	213	
QY	454	tccttcgacacaaagcgtgtctcttggtagagaagtttcagaaacagtcgcgcgaagac	513		Db	121	gacagcgtgactctgactctgactctgactctgactctgactctgactctgactctg	180	
Db	421	tccttcgacacaaagcgtgtctcttggtagagaagtttcagaaacagtcgcgcgaagac	480		QY	214	gtgctcaggaagccggtgcaggctccacccccagcagatgggctgcacatgggaagag	273	
QY	514	ttccagagcgtgcagttatccacagagtcacacaaagtctcttcgacgttagcagtc	573		Db	181	gtgctcaggaagccggtgcaggctccacccccagcagatgggctgcacatgggaag	240	
Db	481	ttccagagcgtgcagttatccacagagtcacacaaagtctcttcgacgttagcagtc	540		QY	274	ctgctgtgagtgctgctgcagtcacacagactctggaaaactattcatctaccggccgc	333	
QY	574	ccgagggagacagctcttctacatagttgcacatgtgcacatgtgcacatgtgcac	633		Db	241	ctgctgtgagtgctgctgcagtcacacagactctggaaaactattcatctaccggccgc	300	
Db	541	ccgagggagacagctcttctacatagttgcacatgtgcacatgtgcacatgtgcac	600		QY	334	cgccacagctggactctgactctgactctgactctgactctgactctgactctgact	393	
QY	634	aaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	693		Db	301	cgccacagctggactctgactctgactctgactctgactctgactctgactctgact	360	
Db	601	aaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	660		QY	394	tgcttcggaagagccctcagcaatgtgttggtagtgggtctctcgaggaccacca	453	
QY	694	aacatcacagtcactgcgttggccagaaaccccgctggctcagttcagttcagttc	753		Db	361	tgcttcggaagagccctcagcaatgtgttggtagtgggtctctcgaggaccacca	420	
Db	754	ccgactcctggaactcatcttctacagactcgtttgagctcagatcagttcagttc	813		QY	454	tccttcgacacaaagcgtgtctcttggtagagaagtttcagaaacagtcgcgcgaag	513	
QY	814	cgttcagaaagacattcacacatgagtgatgcacagcctccagacatcagttgtcat	873		Db	421	tccttcgacacaaagcgtgtctcttggtagagaagtttcagaaacagtcgcgcgaag	480	
Db	873	cgttcagaaagacattcacacatgagtgatgcacagcctccagacatcagttgtcat	840		QY	514	ttccagagcgtgcagttatccacagagtcacacaaagtctcttcgacgttagcagtc	573	
QY	934	gagcgtgagcggcctgagcagcagcagcagcagcagcagcagcagcagcagcag	993		Db	481	ttccagagcgtgcagttatccacagagtcacacaaagtctcttcgacgttagcagtc	540	
Db	901	gagcgtgagcggcctgagcagcagcagcagcagcagcagcagcagcagcagcag	960		QY	574	ccgagggagacagctcttctacatagttgcacatgtgcacatgtgcacatgtgcac	633	
QY	994	cctccagct 1002			Db	541	ccgagggagacagctcttctacatagttgcacatgtgcacatgtgcacatgtgcac	600	
Db	961	cctccagct 969			QY	634	aagtgcagcaaaactcaaacctttcaggggttggaactcttcagcgttagcagtc	693	
RESULT	5				Db	601	aaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag		
5480796-8					QY	694	aacatcacagtcactgcgttggccagaaaccccgctggctcagttcagttcagttc		
Patent No. 5480796					Db	754	ccgactcctggaactcatcttctacagactcgtttgagctcagatcagttcagttc		
APPLICANT: KISHIMOTO, TADAMITSU					QY	814	cgttcagaaagacattcacacatgagtgatgcacagcctccagacatcagttgtcat		
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN					Db	873	cgttcagaaagacattcacacatgagtgatgcacagcctccagacatcagttgtcat		
FOR HUMAN B CELL STIMULATORY FACTOR-2					QY	934	gagcgtgagcggcctgagcagcagcagcagcagcagcagcagcagcagcagcag		
NUMBER OF SEQUENCES: 8					Db	901	gagcgtgagcggcctgagcagcagcagcagcagcagcagcagcagcagcagcag		
CURRENT APPLICATION DATA:					QY	994	cctccagct 1002		
APPLICATION NUMBER: US/07/907,650					Db	961	cctccagct 969		
FILING DATE: 02-JUL-1992									
PRIOR APPLICATION DATA:									
APPLICATION NUMBER: 298,694									
FILING DATE: 19-JAN-1989									
SEQ ID NO:8:									
LENGTH: 1404									

[illegible]

Db 421 CCAACCAATGCGGCTGCTGACGAAGCTGACGACACAGAACAGTGGCTGACGAC 480
 QY 1537 atgacaactcattctgagcagctttaaagagttcctgagtcacagcctgagggct 1596
 Db 481 ATGACAACTCATCTCATCTGCGGAGCTTTAAGGAGTTCTGAGTCCAGCCTGAGGGCT 540
 QY 1597 cttcgcaaatgtag 1611
 Db 541 CTTGGCAAAATGTAG 555

RESULT 8
 US-07-745-382-19
 ; Sequence 19, Application US/07745382
 ; Patent No. 5270181
 ; GENERAL INFORMATION:
 ; APPLICANT: McCoy, John
 ; APPLICANT: Lavallie, Edward
 ; TITLE OF INVENTION: Peptide and Protein Fusions To
 ; TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/745.382
 ; FILING DATE: 19910814
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/652,531
 ; FILING DATE: 06-FEB-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cseri, Luann
 ; REGISTRATION NUMBER: 31,822
 ; REFERENCE/DOCKET NUMBER: G5188A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 876-1170
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 561 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..558
 ; US-07-745-382-19

Query Match 33.8%; Score 550.4; DB 1; Length 561;
 Best Local Similarity 98.9%; Pred. No. 1.3e-127;
 Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1052 tcgagccagtcacccagagagattccaaagattgagccgccccacacagacagccac 1111
 Db 2 TGCGTCCAGTACCTCCAGGTGAGATCTTAAGATGTAGCGCCGCCACACAGACGCCAC 61
 QY 1112 tcacctttcagaacgaattgacaaattcggtacatcctcgagcgcattcagccc 1171
 Db 62 TCACCTCTTCAGAACGAATTGACAAATTCGGTACATCTCTCGAGCGCATCTCAGCCC 121

QY 1172 tgagaagagagacatgtacaagagtagtaacatgtgtgaaagcgcaaaagaggcactggcag 1231
 Db 122 TGAGAAGAGAGACATGTAACAAGAGTAACATGTGTGAAAGCAGCAAAAGAGGACCTGGCAG 181
 QY 1232 aaaaacacctgaaccttccaaagatggctgaaaaagatggatgcttcccaatctggattca 1291
 Db 182 AAAACAACTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCCAATCTGGATTCA 241
 QY 1292 atgagagagacttgctggtgaaatacatcactggctcttttggagtttgagggtataacctag 1351
 Db 242 ATGAGGAGACTTGCCTGGTGAAATCATCACTGGTCTCTTTTGGAGTTTGGATATACCTAG 301
 QY 1352 agtacctcagaacagatttgagtagtagagagaaacacacagcagctgtgcagatagta 1411
 Db 302 AGTACCTCCAGAACAGATTGTAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA 361
 QY 1412 caaaagctcctgacagttcctgcagaaaaagcgaagaatctagatgcaataaccacc 1471
 Db 362 CAAAAGTCTGTATCCAGTTCCTGCAGAAAAAGGCAAAAGATCTAGATGCAATAACCAACC 421
 QY 1472 ctgacccaacacacaaatgcccagcctgctgacgaagtgcagggcacagaaccagtgctgc 1531
 Db 422 CTGACCCACACAAAATGCCAGCTGCTGACGAAGCTGCGAGGCAGACAGAACCAAGCTGCTGC 481
 QY 1532 aggacatgacaactcatctctctctctgagcagctttaaaggagttcctgagctccagctga 1591
 Db 482 AGGACATGACAATCATCTCTCTGCGCAGCTTTAAGGAGTTCTTCCGCTCCAGCCTGA 541
 QY 1592 gggctcttcggcaaatgtag 1611
 Db 542 GGGCTCTTCGCAAAATGTAG 561

RESULT 9
 US-07-921-848-19
 ; Sequence 19, Application US/07921848
 ; Patent No. 5292646
 ; GENERAL INFORMATION:
 ; APPLICANT: McCoy, John
 ; APPLICANT: Lavallie, Edward
 ; TITLE OF INVENTION: Peptide and Protein Fusions To
 ; TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/921.848
 ; FILING DATE: 19920728
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/652,531
 ; FILING DATE: 06-FEB-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,382
 ; FILING DATE: 14-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cseri, Luann
 ; REGISTRATION NUMBER: 31,822
 ; REFERENCE/DOCKET NUMBER: G5188A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 876-1170
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-07-921-848-19

Query Match 33.8%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 1.3e-127;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1052 tcgagccattacccccagagagattccaaagatgtacggcccccacacagacagccac 1111
Db 2 TGCGTCCAGTACCTCCAGTGAAGATTCTAAAGATGTAGCCGCCCCACACAGACGCCAC 61

QY 1112 tcacctcttcagaaagattgacaaattcggtacatcctcgacgcatctcagccc 1171
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTTCGGTACATCTCGACGGCATCTCAGCCC 121

QY 1172 tgagaaagagacatgtacaagagtaacatgtgtgaaagcagcaagagcagtgagcag 1231
Db 122 TGAGAAAGGAGACATGTACAAGAGTAACATGTGTGAAAGCAGCAAGAGGCACCTGGCAG 181

QY 1232 aaaaacacctgaaccttccaaagatgctgaaagagcagcaagagcagtgatctcagattca 1291
Db 182 AAAACAACCTGAACCTTCCAAAGATGCTTCCAAAGATGCTTCCAAATCTGGATTCA 241

QY 1292 atgagagacttgcttggtgaaatcatcactgtctcttttgaggttgaggtatcacctag 1351
Db 242 ATGAGGAGACTTGCTTGTTGAAATCATCATCTGCTTTTGGAGTTGAGGTATACCTAG 301

QY 1352 agtacctccagaacagatttgagagtagtgaggaacaaagcagagctgtgcagatgagta 1411
Db 302 AGTACCTCCAGAACAGATTGAGAGTAGTGAGGAACAAGCAAGAGTGTGCAGATGAGTA 361

QY 1412 caaaagctctgacatctcattctgcgcagctttaagaggttcctgcagtcagcagctga 1591
Db 482 AGGACATGACAACTCATCTCATCTGCGCAGCTTTAAGGAGTTCTGCGAGCTCGAGCTGA 541

QY 1592 gggctcttcggcaaatgtag 1611
Db 542 GGGCTCTTCGGCAAAATGTAG 561

RESULT 10
US-08-165-301A-19
Sequence 19, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBiasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-08-165-301A-19

Query Match 33.8%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 1.3e-127;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1052 tcgagccattacccccagagagattccaaagatgtacggcccccacacagacagccac 1111
Db 2 TGCGTCCAGTACCTCCAGTGAAGATTCTAAAGATGTAGCCGCCCCACACAGACGCCAC 61

QY 1112 tcacctcttcagaaagattgacaaattcggtacatcctcgacgcatctcagccc 1171
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTTCGGTACATCTCGACGGCATCTCAGCCC 121

QY 1172 tgagaaagagacatgtacaagagtaacatgtgtgaaagcagcaagagcagtgagcag 1231
Db 122 TGAGAAAGGAGACATGTACAAGAGTAACATGTGTGAAAGCAGCAAGAGGCACCTGGCAG 181

QY 1232 aaaaacacctgaaccttccaaagatgctgaaagagcagcaagagcagtgatctcagattca 1291
Db 182 AAAACAACCTGAACCTTCCAAAGATGCTTCCAAAGATGCTTCCAAATCTGGATTCA 241

QY 1292 atgagagacttgcttggtgaaatcatcactgtctcttttgaggttgaggtatcacctag 1351
Db 242 ATGAGGAGACTTGCTTGTTGAAATCATCATCTGCTTTTGGAGTTGAGGTATACCTAG 301

QY 1352 agtacctccagaacagatttgagagtagtgaggaacaaagcagagctgtgcagatgagta 1411
Db 302 AGTACCTCCAGAACAGATTGAGAGTAGTGAGGAACAAGCAAGAGTGTGCAGATGAGTA 361

QY 1412 caaaagctctgacatctcattctgcgcagctttaagaggttcctgcagtcagcagctga 1591
Db 482 AGGACATGACAACTCATCTCATCTGCGCAGCTTTAAGGAGTTCTGCGAGCTCGAGCTGA 541

Qy 1592 gggctcttcggc aaatgtag 1611
 |||||
 Db 542 GGGCTCTTCGGCAAATGTAG 561

RESULT 11

PCT-US94-14179-19

Sequence 19, Application PC/TUS94/14179

GENERAL INFORMATION:

APPLICANT: McCoy, John

APPLICANT: DiBloy-Smith, Elizabeth

APPLICANT: Grant, Kathleen

APPLICANT: Lavallie, Edward R.

TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO

TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED

TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14179

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Meinert, M. C.

REGISTRATION NUMBER: 33,544

REFERENCE/DOCKET NUMBER: GI 5188D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 561 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..558

PCT-US94-14179-19

Query Match 33.8%; Score 550.4; DB 6; Length 561;

Best Local Similarity	98.9%;	Prod. NO. 1.3e-127;	0;	Mismatches	6;	Indels	0;	Gaps	0;
Matches	554;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;

Qy	1052	tcgagccagtcacccccaggagaaattccaagaatgtagcgcgcgccacacacagacagccac	1111
Db	2	TGGCTCCAGTACCTCCCAAGTATTCTAAAGATGTAGCGCGCCCCACACAGACGCCAC	61
Qy	1112	tcaccttcagacgaattgacaaacaaattcgggtacatcctcgagcgcatctcagccc	1171
Db	62	TCACCTCTTCAGACGGAATTCACAAACAATTCGGTACATCCTCGACGGCATCTCAGGCC	121
Qy	1172	tgagaaaggagacatgtaaacaagtagtaacatgtgtgaaagcagcaaaagagagcactggcag	1231
Db	122	TGAGAAAGGACATGTAAACAAGAGTAACTGTGTGAAAGCAGCAAGAGGCATCTGGCAG	181
Qy	1232	aaacaacctgaaccttccaaagatggctgaaaagatggatgtctccaattctggattca	1291
Db	182	AAACAACCTCAAGCTTCCAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCA	241

Qy	1292	atagagagacttcgctgggtgaaataatcaactggtgtctttttggagtttgaggtatacactag	1351
Db	242	ATGAGGAGACTTCGCTGGTGAAATCATCACTGGCTTTTGGAGTTTGAGGTATACCTAG	301
Qy	1352	agtaacctccagaacagatttgagagttagtggaaacaagccaagagctgtgcagatgagta	1411
Db	302	AGTACCTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA	361
Qy	1412	caaaagtcctgatccagtttcctgcagaaaaaggcaaaagatactagatgcataaaccacc	1471
Db	362	CAAAAGTCCTGATCCAGTTCCTCGCAAAAAGGCAAAAGTAATCTAGATGCAATAACCAACC	421
Qy	1472	ctgaccaaaccaaatgccagcctgtgcagaaagctgcaggcacagaaaccagtggtctgc	1531
Db	422	CTGACCCACCAACAAATGCCAGCTCTGACCAGACTGCGACACAGAACCAAGTGGCTGCG	481
Qy	1532	aggacatgacaactcatctcatcttcgtcgagctttaaggagttctctgcagttccagctctga	1591
Db	482	AGGACATGACAACATCATCTTCCTGCGCAGCTTTTAAAGGAGTTCCTGCGAGTCCAGCTGA	541
Qy	1592	gggctcttcggcaaatgtag	1611
Db	542	GGGCTCTTCGGCAAAATGTAG	561

RESULT 12

```

US-08-469-318-57
Sequence 57, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 951 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-318-57

```

Query Match	33.1%	Score 539.2;	DB 5;	Length 951;
Best Local Similarity	94.4%;	Pred. No. 8,9e-125;		
Matches 559;	Conservative	0;	Mismatches 33;	Indels 0;
Gaps	0;			

Qy	1017	tctgagagtgagaggtcttgagagtgagaggtctctgagccagtcaccccgagagaga	1076
Db	360	TTCCCGGGTGTGTGTTCTGGCGCGGGTCCAAACATGGCTCCAGTACCACCGAGTGA	419
Qy	1077	ttccaaagatgtagcgcgccccacacagacagccactcacctcttcagaacgaattgacaa	1136
Db	420	TTCCAAGATGTGGCGCGCCACACAGACAGCCACTACCTCTTCAGAACGAATTGACA	479
Qy	1137	acaaattcgttacatcctcgacgcatctcagccctgagaagagacatgtaacaagag	1196
Db	480	ACAAATTCGGTACATCTCGACGGGATATCAGCCCTGAGAAGGAGACATGTACACAG	539
Ov	1197	taacatctctgaaagcagcaagagagcactggcagaaacaaacctgaaccttccaaagt	1256

Db 540 TAACATGTGTGAAGCAGCAAAAGAGCGCTAGCAGAAAAACAACCTGAACCTTCCAAAGAT 599
QY 1257 gctgaaaaagatgattcctcaatcttgattcaatgagagacttgctggtgaaat 1316
Db 600 GCGTGAAGAAAGATGGATGCTTCCATCCGGATTCATAGGAGACTTGCTGGTGAAT 659
QY 1317 catcactgctctttggagttgaggtatcacctagtagtaccctccagaaacagattgagag 1376
Db 660 CATCACTGGTCTTTGGAGTTTGAGGTATACCTCGAGTACCTCCAGAACAGATTGAGAG 719
QY 1377 tagtgaggaaacagcagctgtgcagatgagtaacaaagtctcgatccagttctcgca 1436
Db 720 TAGTGAGGAACAAAGCAGAGCTGTGCAGATGTGCAAAAGTCTGATCCAGTTCCTGCA 779
QY 1437 gaaaaggcaaaagatctagatgcaataaccacccctgaccccaacacaaatgccagcct 1496
Db 780 GAAAAGGCAAAAGATCTAGATGCAATAACCAACCCCTGACCCCAACCAAAATGCATCCT 839
QY 1497 gctgacgaagctgcaggcacagaaacagtggtgcagagacatgacaaactcatctattct 1556
Db 840 GCTGACGAAGCTGCAGGCACAGACAGTGGCTGCAGGACATGACAACCTCATCTCATCT 899
QY 1557 ggcgagctttaaggagttctcagtcagtcagcctgagggctcttcggcaaatg 1608
Db 900 GCGCAGCTTTAAGGAGTTCTCTGAGTCCAGCCTGAGGGCTCTTCGGCAAAATG 951

RESULT 13

PCT-US95-01185-57

; Sequence 57, Application PC/TUS9501185

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion

; TITLE OF INVENTION: Protein

; NUMBER OF SEQUENCES: 196

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/01185

; FILING DATE: 02-FEB-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/192325

; FILING DATE: 14-FEB-1994

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 951 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

PCT-US95-01185-57

Query Match

Best Local Similarity 33.1%; Score 539.2; DB 6; Length 951;

Matches 559; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1017 ttctggagtgaggttctcaggtggaggttctcagcagcagtcaccccaaggagaaga 1076
Db 360 TTCCCGGGTGTGGTTCTTGGCGGGCTTCCAAATGCTCAGTACCCAGGTTGAAGA 419
QY 1077 ttccaaagatgtagcgcgcacacagacagccactcactcttcagaaacgaattgacaa 1136
Db 420 TTCCAAAGATGTGGCGGGCCCCACACAGACAGCCACTCACCCTTTTCAGAACGAATTGACAA 479
QY 1137 acaattcgggtacatctctcagcgggcatctcagccctgagaaggagacatgtacaagag 1196
Db 480 ACAAAATTCGGTACATCTCTCGACGGGATATACGCCCTGAGAAAGGAGACATGTAAACAAGAG 539

QY 1197 taacatgttgaagcagcaaaagcactggcagaaaaacaacctgaacattccaagat 1256
Db 540 TAACATGTGTGAAGCAGCAAAAGAGCGCTAGCAGAAAAACAACCTGAACCTTCCAAAGAT 599
QY 1257 gctgaaaaagatgattcctcaatcttgattcaatgagagacttgctggtgaaat 1316
Db 600 GCGTGAAGAAAGATGGATGCTTCCATCCGGATTCATAGGAGACTTGCTGGTGAAT 659
QY 1317 catcactgctctttggagttgaggtatcacctagtagtaccctccagaaacagattgagag 1376
Db 660 CATCACTGGTCTTTGGAGTTTGAGGTATACCTCGAGTACCTCCAGAACAGATTGAGAG 719
QY 1377 tagtgaggaaacagcagctgtgcagatgagtaacaaagtctcgatccagttctcgca 1436
Db 720 TAGTGAGGAACAAAGCAGAGCTGTGCAGATGTGCAAAAGTCTGATCCAGTTCCTGCA 779
QY 1437 gaaaaggcaaaagatctagatgcaataaccacccctgaccccaacacaaatgccagcct 1496
Db 780 GAAAAGGCAAAAGATCTAGATGCAATAACCAACCCCTGACCCCAACCAAAATGCATCCT 839
QY 1497 gctgacgaagctgcaggcacagaaacagtggtgcagagacatgacaaactcatctattct 1556
Db 840 GCTGACGAAGCTGCAGGCACAGACAGTGGCTGCAGGACATGACAACCTCATCTCATCT 899
QY 1557 ggcgagctttaaggagttctcagtcagtcagcctgagggctcttcggcaaatg 1608
Db 900 GCGCAGCTTTAAGGAGTTCTCTGAGTCCAGCCTGAGGGCTCTTCGGCAAAATG 951

RESULT 14

PCT-US94-12873-3

; Sequence 3, Application PC/TUS9412873

; GENERAL INFORMATION:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; TITLE OF INVENTION: HYBRID CYTOKINES

; NUMBER OF SEQUENCES: 26

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density

; COMPUTER: AST-IBM Compatible

; OPERATING SYSTEM: MS-DOS Version 6

; SOFTWARE: WORD for WINDOWS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/12873

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 540

; TYPE: nucleic acid

; STRANDEDNESS: double stranded

; TOPOLOGY: linear

PCT-US94-12873-3

Query Match

Best Local Similarity 33.1%; Score 538.4; DB 6; Length 540;

Matches 539; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1072 gaagattccaaagatgtagcccccacacagacagccactcacctcttcagaaacgaatt 1131
Db 1 GAAGATTCCAAAGATGTAGCCGCCCCACACAGACGCCACTCACCTTTCAGAACGAAT 60
QY 1132 gacaaacaaattcgggtacatcctcagcggcatctcagccctgagaaaggagacatgtaac 1191
Db 61 GACAAACAAATTCGGTACATCTCTCGAGCGCATCTCAGCCCTGAGAAAGGAGACATGAAC 120
QY 1192 aagagtacaatgtgaaagcgcaaaaggcactggcagaaaaaacacactgaacctcca 1251
Db 121 AAGAGTAACATGTGTGAAAGACGACAAAGAGGACTGGCAGAAAAACCAACCTGAACCTTCCA 180
QY 1252 aagatggctgaaaaagatggatgcttccaatctggattcaatgaggagacttgctgggtg 1311

Db 181 AAGATGGCTGAAAGAGTGAATGCTTCAATCTGGATTCATGAGGAGACTTGCTCGTG 240
Qy 1312 aaatcatcactgctcttttggagtttgagtgatatacctagtagtacctccagaaacagattt 1371
Db 241 AAATCATCACTGCTCTTTTGGAGTTTGAGGTATACCTAGAGTACCTCCAGAACAGATTT 300
Qy 1372 gagagtgtaggagaaagccagagctgtgcagatgagtagacaaagtcctgatccagttc 1431
Db 301 GAGAGTAGTAGGAGAACAGCCAGAGCTGTCCAGATGAGTACAAAGTCCCTGATCCATTC 360
Qy 1432 ctgcagaaaaagccaaagatcttagatgcaataaccacccctgaccccaaccacaaatgcc 1491
Db 361 CTCGAGAAAAGGCAAGAAATCTAGATGCAATACCACTGACCCCAACCAAAATGCC 420
Qy 1492 agcctgtgcagaaagctgcaggccagacagacagctggctgcaggacatgacaactcatctc 1551
Db 421 AGCCTGTGAGGAAGCTGCAGGCACAGAACAGTGGCTGCAGGACATGACAACATCATCTC 480
Qy 1552 attctgcagactttaaggagttcctcagtcagtcagcctgaggctcttcggcaaatag 1611
Db 481 ATTCTGCGACGCTTAAGGAGTTCTCTGAGTCCAGCTGAGGGCTCTTCGGCAAAATGTAG 540

RESULT 15

US-08-567-047-1
; Sequence 1, Application US/08567047
; Patent No. 5789552
; Patent No. 5789552 5789555
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; APPLICANT: CILIBERTO, Gennaro
; TITLE OF INVENTION: METHOD FOR SELECTING SUPRAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPRANTAGONISTS FOR HORMONES HAVING
; TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,047
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,924
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: IT RM93A000409
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SAVINO=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; LIBRARY: production in bacteria
; FEATURE:
; NAME/KEY: IL-6 cDNA
; IDENTIFICATION METHOD: polyacrylamide gel
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..552
; US-08-567-047-1

Query Match 32.9%; Score 535.8; DB 2; Length 555;
Best Local Similarity 97.8%; Pred. No. 5.2e-124; Indels 0; Gaps 0;
Matches 543; Conservative 0; Mismatches 12;

Qy 1057 ccagtacccccagagagattccaaagatgtagcccccacacacagacagccactcaac 1116
Db 1 CCAGTACCCCCAGGAGAGATTCCAAAGATGTAGCCGCCCCACACACAGACAGCCACTCAGG 60
Qy 1117 tcttcagaacgaattgacaaataattcggtacatctcctcagcggcatctcagccctgaga 1176
Db 61 AGCTCAGAACGAATTGACAAATAATTCGGTACATCTCGACGGCATCTCAGCCTTAAGA 120
Qy 1177 aaggagacatgtaacagagtagtaacatgtgtgaagcagcaaaagagcactggcgagaaac 1236
Db 121 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAGAGGACTGGCAGAAAAAC 180
Qy 1237 aacctgaaccttccaaagatggctgaaagagtgatgtctccaaatctggattcaatgag 1296
Db 181 AACCTGAACCTTCCAAAGATGGCTGAAAGATGGATGCTTCCAAATCTGGATTCAATGAG 240
Qy 1297 gagacttgctgggtgaaataatcactgggttttttgaggtttgaggtatacctagagtac 1356
Db 241 GAGACTTGCTGGTGGTGAATAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 300
Qy 1357 ctccagaacagatttgagagtagtgaggaacaagccagagctgtgcagatgagtcacaaaa 1416
Db 301 CTCCAGAACAGATTTGAGAGTAGTAGAGGAACAAGCCAGAGCTGTCCAGATGAGTACAAAA 360
Qy 1417 gtctgatccagttcctgcagaaaaagcaagaatctagatgcaataaccacccctgac 1476
Db 361 GTCCTGATCCAGTTCTCTGCAGAAAAAGGCAAGAAATCTAGATGCAATAAACCCCTGAC 420
Qy 1477 ccaaccacaaatgcagcctctgcagaaagctgcagacagacagacagagtgctcgagac 1536
Db 421 CCAACCACAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCACTGGCTGCAGGAC 480
Qy 1537 atgacaactcatctcattctgcgcagctttaaggagttcctgcagtcagcctgagggct 1596
Db 481 ATGACAACTCATCTCATTTCTGAGATCTTTTAAGGAGTTCTCTGCAGTCCAGCTCAGGGCT 540
Qy 1597 cttcggcaaatgtag 1611
Db 541 CTTGGCAAAATGTAG 555

Search completed: August 9, 2000, 09:32:39
Job time: 35080 sec

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1627	100.0	1627	1	T97848	Human fusion polyp	
2	1457	89.6	1552	1	T97849	Human fusion polyp	
3	995	61.2	2061	1	N90340	Sequence encoding	
4	995	61.2	2066	1	Q41746	IL-6 receptor codi	
5	995	61.2	2087	1	N08047	DNA contg. region	
6	995	61.2	3319	1	V60295	Human interleukin-	
7	993.4	61.1	1486	1	V60295	Human interleukin-	
8	993.4	61.1	3319	1	T31441	Interleukin-6 rece	
9	969	59.6	1074	1	V04440	Interleukin 6 rece	
10	565.2	34.7	1139	1	N80255	Interleukin-6. New	
11	565.2	34.7	1139	1	N80299	Interleukin 6. Pro	
12	565.2	34.7	1162	1	Q01763	BSF-2 gene for hum	
13	563.6	34.6	1101	1	N90131	DNA sequence of pB	
14	563.6	34.6	1101	1	N90135	DNA sequence of pB	
15	563.6	34.6	1101	1	N90345	Plasmid pBSF2-L8	
16	563.6	34.6	1128	1	Q74057	Human interleukin-	
17	563.6	34.6	1128	1	V60294	Human interleukin-	
18	563.6	34.6	1145	1	N90377	Interferon-beta-2	
19	563.6	34.6	1145	1	N70348	Sequence of human	
20	563.6	34.6	1145	1	Q39582	IFN-beta-2a coding	
21	563.6	34.6	1145	1	Q86523	cDNA encoding inte	
22	563.6	34.6	1161	1	N81460	Sequence encoding	
23	562	34.5	1101	1	N80965	Plasmid pBSF2-L8.	
24	562	34.5	1101	1	N81517	Sequence encoding	
25	558.8	34.3	1099	1	Q25831	Mutant human BCDF	
26	558	34.3	1165	1	Q56265	Sequence of human	
27	555	34.1	639	1	N91706	Human interleukin-	
28	554	34.1	1162	1	Q11824	B cell differentia	
29	552.2	33.9	566	1	N80300	Interleukin 6. Pro	
30	551.8	33.9	555	1	Q85465	Mutant Interleukin	
31	550.4	33.8	561	1	Q36903	Human Interleukin	
32	550.4	33.8	561	1	Q30773	Human Interleukin	
33	549	33.7	560	1	Q03365	Segment of human B	

PS Disclosure; Fig 3; 63pp; English.
CC The cDNA in N90340 was derived from monocyte cell line U937.
CC Isolated BSE2 receptor and DNA encoding it are claimed, as are
CC (b) expression vectors; (c) host organisms; (d) antibodies; and
CC (e) hybridomas.
SQ Sequence 2061 BP; 418 A; 631 C; 621 G; 391 T;

```
Query Match          61.2%; Score 995; DB 1; Length 2061;
Best Local Similarity 100.0%; Pred. No. 6.8e-242;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 catgagtggttagccgaggaagacatgctgcccgtcgctgcgctgcgctgctgctccc 67
    |||
Db 221 CATGAGTGGTAGCCGAGGAGACATGCTGGCCGTCGGCTGCGCTGCTGCTGCTGCC 280

Qy 68 tgcctgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 127
    |||
Db 281 TGCTGGCCGCGCGGAGCGGCTGGCCGCCAAGCGCTGCTGCTGCGCAGGAGTGCAA 340

Qy 128 gagcgctgctaccagctgctgcagagagacagctgaactctgaacctgcccgggtagagc 187
    |||
Db 341 GAGGCGTGTCTACCACTGTGCGAGGAGACAGCTGACTCTGACCTGCGCCGGGGTAGAGC 400

Qy 188 cgaagacaatgcacactttcactgggtgctcaggaagccgctgcaggtcccccacccca 247
    |||
Db 401 CGGAAGACAATGCCACTGTTCACTGGGTGCTCAGGAAGCCGCTGCAGGCTTCCACCCCA 460

Qy 248 gcatatgctgctgagtgaggaagagctgctgctgaggtcggtgcagctccacactctg 307
    |||
Db 461 GCAGATGGCTGGCATGTGGAAGAGGCTGCTGCTGAGTGTGCTGAGTCCACGACTCTG 520

Qy 308 gaaactatcatgctaccagctgctgcagagagacagctgaactctgctgctgctgctg 367
    |||
Db 521 GAAACTATTCATGCTACCGGCGCGCCGCGCAGCTGGGACTGTGCACTGTGCTGGGATG 580

Qy 368 ttccccccgagagccagctctctctctctcgcgaagagcccccagcaatgtgtttt 427
    |||
Db 581 TTCCCCCGGAGGAGCCAGCTCTCTCTGCTCCGGAAGAGCCCCCTCAGCAATGTGTTT 640

Qy 428 gtgagtggtgctcctgagagaccccatcctctgacgacaaagagctgtctgtgtgagga 487
    |||
Db 641 GTGAGTGGGGTCTCTGGAGACACCCATCCCTGACGACAAAGGCTGTGCTTGTGTGAGGA 700

Qy 488 agttcaaacagctccgcccgaagacttccagagccgtgcccagctatcccagagagctcc 547
    |||
Db 701 AGTTTTCAGAACAGTCCGGCCGAAGACTTCCAGAGCCGCTGCCAGTATTCACGAGAGTCC 760

Qy 548 agaagtctctcctgccagtttagcagttcccgagggagagacagctcttctacatagtcca 607
    |||
Db 761 AGAAGTTCTCTCCAGTGTAGCAGTCCCGGAGGAGAGACAGCTCTTCTTACATAGTGCCA 820

Qy 608 tgtgctgcagagtagtgcggagcaagttcagcaaaactcaaaccttcaaggttatg 667
    |||
Db 821 TGTGCTGCCAGTAGTGTGCGGAGCAAGTTACGAAAAACTCAAACTTTCAGGGTTGTG 880

Qy 668 gaactctgagctgactccgctgcaacatcacagctactccgtggcagaaaccccc 727
    |||
Db 881 GAATCTTGACGCTGATCGCTGCCACATCACAGTCACTGCTGCGGCGCAGAAACCCCC 940

Qy 728 gctggtcagtgctacactggcagacccccactcctctggaactcatcttctcagactac 787
    |||
Db 941 GCTGGCTCAGTGTACCTGGCAAGACCCCACTCTCTGGAACATCATCTTCTACAGACTAC 1000

Qy 788 ggtttgagctcagatagctgggtgaacgtcaagacattcaacatgagtggtcaagg 847
    |||
Db 1001 GGTTTGAGCTCAGATATCGGGTGAACAGGTCAAGACATTCACAACTGGATGGTCAAGG 1060

Qy 848 acctcagactactgtgtcattccagcgcctggagggcctgagcgacgtggtgacgc 907
    |||
Db 1061 ACCTCAGCATCATCTGTGTATCCAGCGCTGGAGCGGCTGAGGACAGTGGTGACG 1120

Qy 908 ttcgtgcccagggaggttcgggcaaggcgagtgagagcgagtgaggccccggagccatgg 967
    |||
```

```
Db 1121 TTCTGCCAGGAGGAGTTCCGGCAAGGCGAGTGGAGCGAGTGGAGCCGAGGCCATGG 1180
    |||
Qy 968 gcaacgcttgacagaatccaggagctccacgt 1002
    |||
Db 1181 GCACGCTTGGACAGAATCCAGGAGTCTCTCCAGCT 1215

RESULT 4
Q41746
ID Q41746 standard; DNA; 2066 BP.
AC Q41746;
DT 13-SEP-1993 (first entry)
DE IL-6 receptor coding sequence.
KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
KW transmembrane; multiple myeloma; binding; ability; signal transfer;
KW disease; intracellular; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 226..1632
    /*tag= a
FT J05001892-A.
PN 16-APR-1993.
PF 02-OCT-1991; 255521.
PR 02-OCT-1991; JP-255521.
PA (CHUS ) CHUGAI PHARM CO LTD.
PA (KISH/) KISHIMOTO C.
PA (TOYJ ) TOSOH CORP.
DR WPI; 93-161739/20.
DR P-PSDB; R37215.
PT New interleukin-6 receptor deriv. - for treating diseases caused
    by IL-6, e.g. multiple myeloma
PS Disclosure; Page 10-12; 23pp; Japanese.
CC This sequence encodes an interleukin-6 (IL-6) receptor. Variants of
    the receptor lacking either the immunoglobulin-like domain or the
    transmembrane and intracellular domain have IL-6 binding ability and
    signal transfer ability. Either the full length or truncated IL-6
    receptors may be used for diseases caused by IL-6 such as multiple
    myeloma.
CC Sequence 2066 BP; 420 A; 642 C; 615 G; 389 T;
```

```
Query Match          61.2%; Score 995; DB 1; Length 2066;
Best Local Similarity 100.0%; Pred. No. 6.8e-242;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 catgagtggttagccgaggaagacatgctgcccgtcgctgcgctgcgctgctgctccc 67
    |||
Db 200 CATGAGTGGTAGCCGAGGAGACATGCTGGCCGTCGGCTGCGCTGCTGCTGCC 259

Qy 68 tgcctgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 127
    |||
Db 260 TGCTGGCCGCGCGGAGCGGCTGGCCGCCAAGGCGCTGCTGCTGCGCAGGAGTGCAA 319

Qy 128 gagcgctgctaccagctgctgcagagagacagctgaactctgacctgcccgggtagagc 187
    |||
Db 320 GAGGCGTGTCTACCACTGTGCGAGGAGACGCTGACTTCACTGCTGCCGGGGTAGAGC 379

Qy 188 cgaagacaatgcacactgttcaactgttgcctgaggaagccgctgcaaggtcccccaccca 247
    |||
Db 380 CGGAAGACAATGCCACTGTTCACTGGGTGCTCAGGAAGCCGCTGCAGGCTTCCACCCCA 439

Qy 248 gcatatgctgctaccagctgctgcagagagacagctgaactctgctgctgctgctgctg 307
    |||
Db 440 GCAGATGGCTGGCATGTGGAAGAGGCTGCTGCTGAGTGTGCTGAGTCCACGACTCTG 499

Qy 308 gaaactatcatgctaccagctgctgcagagcccccagctgggagctgcaactgtggtgagtg 367
    |||
Db 500 GAAACTATTCATGCTACCGGCGCGCCCGCCAGCTGGGACTGTGCACTTGTGTTGGATG 559

Qy 368 ttccccccgagagccagctctctctgcttcccgaaagagccccctcagcaatgtgttt 427
    |||
Db 560 TTCCCCCGGAGGAGCCAGCTCTCTCTGCTCCGGAAGAGCCCCCTCAGCAATGTGTTT 619
```


QY	968	gcacgcttgacagaatccaggagtgctccagct 1002	
Db	1181	GCACGCTTGACAGATCCAGGAGTCTCCAGCT 1215	
RESULT 6			
V60295			
ID	V60295	standard; DNA; 3319 BP.	
AC	V60295		
DT	02-FEB-1999	(first entry)	
DE	Human interleukin-6 receptor cDNA.		
KW	Interleukin-6 receptor; human; hepatitis B virus; HBV; infection; therapy; ss.		
OS	Homo sapiens.		
PN	W09835694-A2.		
PD	20-AUG-1998.		
PF	10-FEB-1998; U08898.		
PR	11-FEB-1997; US-795473.		
PA	(DAVI/) DAVIDSON C M.		
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.		
DR	WPI; 98-520755/44.		
PT	treatment of hepatitis B virus infection - using a soluble active agent which prevents interaction of HBV with hepatocytes mediated by human interleukin 6		
PT	human interleukin 6		
PS	Disclosure; Fig 6a-b; 5lpp; English.		
CC	This is a previously reported nucleotide sequence for human interleukin-6 (hIL-6) receptor mRNA. The invention relates to the finding that hIL-6 is essential for hepatitis B virus (HBV) infection. The invention provides a pharmaceutical composition for the treatment of HBV infection, comprising a soluble active agent that interacts with at least one of the binding sites between hIL-6 and the p51 region of HBV and between hIL-6 and hepatocytes and other HBV-permissive cells. The active agent competitively binds to at least one of these sites and thereby prevents hIL-6-mediated HBV infection of hepatocytes and other HBV-permissive cells. The soluble active agent is selected from glycoprotein 80 (gp80) having receptor sites which interact with hIL-6, soluble glycoprotein 130 (gp130) having receptor sites which interact with hIL-6, hIL-6 derived peptide Lys41-Ala56, hIL-6 derived peptide Gly77-Glu95, hIL-6 derived peptide Gln153-His165, a combined 1 and 2 hIL-6 mutant (mHIL-6 1+2), and mHIL-6 1+2 substituted with Phe171 to Leu and Ser177 to Arg, and mixtures of any of these.		
CC	and Ser177 to Arg, and mixtures of any of these.		
CC	Sequence 3319 BP; 735 A; 936 C; 687 T;		
SEQ			
Query Match 61.2%; Score 995; DB 1; Length 3319;			
Best Local Similarity 100.0%; Pred. No. 8.2e-242;			
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	8	catgagatgtagccagaggaagcatgctgcccgtcgctgcgctgctgctgctgccc 67	
Db	412	CATGGAGTGTGATGCGAGGAGGAGCATGCTGCGCGTGGCTGCGCGTGGCTGCC 471	
QY	68	tgtctgcccgcgcggagcggcgctggcccgaagcgctgcccgtcgagggagggtgca 127	
Db	472	TGCTGCGCGCGCGGAGCGCGCTGGCCCAAGGCGCTGCCCTGCGAGGAGGTGGCAA 531	
QY	128	gagcgctgtagcagatctgcagagagacagtgactctgactctgactctgcccgggtagagc 187	
Db	532	GAGGCGTGTGACCACTGTGCCAGGAGAGCGGTGACTCTGACCTGCCGGGGGTAGAC 591	
QY	188	cgaagacaaatgcactgttctactggtgtgctcaggaagcggctgagggctcccaccca 247	
Db	592	CGAAGACATGCCACTGTCTACTGGTGTCTCAGGAAGCGGCTGCAGGCTCCACCCCA 651	
QY	248	gcagatgggctggcaggaagagctgctgtaggctgctgtaggctgtaggctgtaggctg 307	
Db	652	GCAGATGGGCTGGGAGGAGGCTGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTG 711	
QY	308	gaactattcatctaccggcgccgcgcagctgggactgtgcaacttgctggtgtagtg 367	
Db	712	GAACATATTCACTACCG 771	

QY	368	ttccccccgag 427	
Db	772	TTCCCCCAGGAG 831	
QY	428	gtgagtggtggtctctgag 487	
Db	832	GTGAGTGGGGTCTCTGGAG 891	
QY	488	agtttcag 547	
Db	892	AGTTTTCAG 951	
QY	548	aaagttctctgag 607	
Db	952	AGAAGTTCCTCTGAG 1011	
QY	608	tgtgctgctgag 667	
Db	1012	TGTGCTGCGCAGTAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1071	
QY	668	gaatttcag 727	
Db	1072	GAATTCGAG 1131	
QY	728	gctggtcag 787	
Db	1132	GCTGGCTCAGTGTGCTGAG 1191	
QY	788	ggttgagctcag 847	
Db	1192	GGTTGAGCTCAGATATCGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1251	
QY	848	acctcag 907	
Db	1252	ACCTCAG 1311	
QY	908	ttcgtgcccag 967	
Db	1312	TTCTGTCGCGAGGAG 1371	
QY	968	gcagccttgag 1002	
Db	1372	GCAGCCTTGAG 1406	
RESULT 7			
V60296			
ID	V60296	standard; DNA; 1486 BP.	
AC	V60296		
DT	02-FEB-1999	(first entry)	
DE	Human interleukin-6 nucleotide sequence.		
KW	Interleukin-6; human; hepatitis B virus; HBV; infection; therapy; ss.		
OS	Homo sapiens.		
PN	W09835694-A2.		
PD	20-AUG-1998.		
PF	10-FEB-1998; U08898.		
PR	11-FEB-1997; US-795473.		
PA	(DAVI/) DAVIDSON C M.		
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.		
DR	WPI; 98-520755/44.		
PT	treatment of hepatitis B virus infection - using a soluble active agent which prevents interaction of HBV with hepatocytes mediated by human interleukin 6		
PT	human interleukin 6		
PS	Disclosure; Fig 7; 5lpp; English.		
CC	This is a previously reported nucleotide sequence for human interleukin-6 (hIL-6). The invention relates to the finding that hIL-6 is essential for hepatitis B virus (HBV) infection. The invention provides a pharmaceutical composition for the treatment of HBV infection, comprising a soluble active agent that interacts with at least one of the binding sites between hIL-6 and the p51 region of HBV and between hIL-6 and hepatocytes and other HBV-permissive cells. The active agent competitively binds to at		

|||||
712 GAAACTATTATGCTACCGGGCGGGCGCCAGCTGGAGCTGTGCACCTGCTGCTGGATG 771
368 ttccccccgagagagccagctctctcgttccggaagagcccccctcagcaatgtgttt 427
772 TTCCCGCGAGAGCCCGCAGCTCTCTGCTTCCGGAAGAGCCCGCTCAGCAATGTTGTT 831
428 gtgagtggggtcctcgagcaaccctcctcgacgacaaaggctgtgtctttggtgagga 487
832 GTGAGTGGGGTCTCGGAGCACCCCATCTCTGAGACAAAAGGCTGTGCTCTGGTGAGGA 891
488 agtttcagaaacatccgagcaaaccttcaggagcgtgcccagattccacagagtc 547
892 AGTTTCAGAACAGTCCCGGCCGGAACATCTCCAGGAGCCGTCGCCAGTATTCACGAGTCCC 951
548 aagaattctctgcagttagtcagtcacagtcagtcagtcagtcagtcagtcagtcagtc 607
952 AGAAGTCTCTCGGAGTACAGTCCCGGAGGAGGAGCAGCTCTTCTACATAGTGCCA 1011
608 tgtggtcgccagtagtgtcggggaagttcagcaaaactcaaaccttttcaggtgttg 667
1012 TGTGCGTCCGAGTAGTGTGCGGAGCAAGTTTCAGCAAAACTCAAACTTTTCAGGGTTGTG 1071
668 gaatttcagacgtatccgctgcccacatcacagtcagtcagtcagtcagtcagtcagtc 727
1072 GAATCTTGAGCCTGATCCGCTGCCACATCACAGTCACTGCGGTGCCAGAAACCC 1131
728 gctgctcagtgctacgtggaagacccccactcctggaactcattctttacagactac 787
1132 GCTGCTCAGTGTACCTTGGCAAGACCCCACTCTCTGGAACATCATCTTTACAGACTAC 1191
788 gtttgagctcagatagtggtgagtcagtcagtcagtcagtcagtcagtcagtcagtc 847
1192 GGTGTTGAGTCAAGTATCGGGCTGAACCGTCAAGCAATTCACACATGATGTCRAAG 1251
848 acctccagatcacgtgtctatccacgacgctgagcgagcgagcgagcgagcgagcgagc 907
1252 ACCTCCAGCATCAGTGTGTCATCCACGACGCGCTGGAGCGGCTGAGGACGCTGTCAGC 1311
908 ttctgccccagagagtagtcggggaagcgagtcagtcagtcagtcagtcagtcagtcagtc 967
1312 TTCTGCTCCCGAGGAGTTCGGGCAAGCGGAGTGGAGCGAGTGGAGCGCGCGGAGGCGCATGG 1371
968 gcaacgcttgagcagaatccaggagtcctccagct 1002
1372 GCACGCTTGGACAGAAATCCAGGAGTCTCTCCAGCT 1406

RESULT 9
V04440
ID V04440 standard; DNA; 1074 BP.
AC V04440;
DT 27-APR-1998 (first entry)
DE Interleukin 6 receptor DNA.
KW Interleukin 6 receptor; human; screening;
KW combinatorial library; ss.
OS Homo sapiens.
PN W0973720-1.
PD 09-OCT-1997.
PR 02-APR-1997; U05821.
PR 03-APR-1996; US-627151.
PA (CHUG-) CHUGAI BIOPHARMACEUTICALS INC.
PI Becherer KA, Brown SJ, Spinella DG;
DR WPI; 97-503233/46.
PT Screening of compounds for ability to bind specific molecules -
PT using a chimeric protein in which the specific molecule is fused to
PT an immunoglobulin chain
PS Example 5; Pages 39-40; 80pp; English.
CC The present sequence was used in the development of a novel method
CC of screening compounds for ability to bind a specific molecule. The
CC method comprises contacting one or more compounds with a chimeric
CC protein containing at least two domains, the 1st comprising a
CC portion of the specific molecule, and the 2nd an immunoglobulin

CC chain portion having one or more epitopes and/or immunoglobulin
CC regions recognising an epitope. A binding partner complex between
CC the chimeric protein and compound(s) is formed, separated out and
CC contacted with a (in)directly labelled secondary molecule which
CC binds the 2nd domain, and the label detected. Using the chimeric
CC proteins, compounds can be rapidly screened for binding to an
CC antigen, antibody, enzyme, substrate, receptor or ligand,
CC e.g. in biomedical research and drug development. The method is
CC especially intended for screening combinatorial libraries, but is
CC also useful in screening bacterial/phage lysates, assays requiring
CC specific binding partner interaction and obtaining binding
CC analogues of a compound.
SQ Sequence 1074 BP; 223 A; 321 C; 324 G; 206 T;
Query Match 59.6%; Score 969; DB 1; Length 1074;
Best Local Similarity 100.0%; Pred. No. 1.9e-235;
Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 34 atgtcgccgtcggtcgctgctggtgctgctgctgctgctgctgctgctgctgctgctgctg 93
Db 1 ATGCTGGCGTGGCTGCGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG 60
QY 94 gccccaaaggcgctgcccgtcgccaggggtggcaaggcgctgctgctgctgctgctgctgctg 153
Db 61 GCGCCAAAGGCGCTGCCCTGCGCAGAGGAGTGGCAAGAGGCGTGGCTGACCAAGTGCCTG 120
QY 154 gacagcgtgactgactgactgactgactgactgactgactgactgactgactgactgactgact 213
Db 121 GACAGCTGACTCTGACCTGCCCGGGGTAGAGCCGGAAGACAATGCCACTGTTCACTGG 180
QY 214 gtgctcaggaagcggtcgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 273
Db 181 GTGCTCAGGAAGCGGCTGCAGGCTCCACCCAGCAGATGGGCTGGCATGGGAAGAGG 240
QY 274 ctgctcgtgagtcggtcgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 333
Db 241 CTGCTGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
QY 334 cgccccagctgggactgtgactgtgctgctgctgctgctgctgctgctgctgctgctgctg 393
Db 301 CGCCCGAGCTGGGAGTGTGCATTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
QY 394 tgcctcgggaagagcccccctcagcaatgtgtgtgagtggtggtggtggtggtggtggtggt 453
Db 361 TGCTTCGGGAAGAGCGCCCTCAGCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 420
QY 454 tccctgacgacaaaggctgtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 513
Db 421 TCCCTGACGACAAAGGCTGTGCTCTTGTGTGAGGAAGTTTCAGAACAGTCCGCGCGCAAG 480
QY 514 ttccaggagccgtgcccagtagtattcccccagagagtcacagagagttctcctccagttagc 573
Db 481 TTCCAGGAGCGGTGCCAGTATTCAGAGAGTCCAGAGTTCCTCTGCTCCAGTATGACAGTC 540
QY 574 ccgagagagacagctcttctacatagtcctcagtcgctgctgctgctgctgctgctgctgct 633
Db 541 CCGGAGGAGAGACAGCTCTTTCTACATAGTTCATGTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 634 aagttcagcaaaactcaaacctttcaggggtgtggaatcttgagcgtgctgctgctgctgctg 693
Db 601 AAGTTTCAGCAAAACTCAAACTTTTCAGGGTGTGTGGAATCTTTCAGAGCTGTATCCCGCT 660
QY 694 aacatcagagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 753
Db 661 AACATCACAGTCACTGCGCTGGCCAGAAACCCCGCTGGCTCAGTGTGCTCCTGCTGCTGCA 720
QY 754 cccactcctggaactcatcttctacagactacggttttgagctcagatatcggtcgtaa 813
Db 721 CCCCACTCTCTGGAATCATCTTCTACAGACTACGCTTGGTGGTGGTGGTGGTGGTGGTGG 780
QY 814 cgggtcaagacattcacacatggtggtcagggacctccagcagtcagtcagtcagtcagtc 873

Qy	1417	gtctgtatccagttcttcgcagaaaaaggcaagaatcttagtgcataaccacccctgac	1477
Db	495	gtctgtatccagttcttcgcagaaaaaggcaagaatcttagtgcataaccacccctgac	554
Qy	1477	ccaaccacaatcccagctgctgcagaaagctgcaggcacagaaacagctggctcaggac	1536
Db	555	ccaaccacaatgccaagcttgcctgcagaaagctgcaggcacagaaacagctggctcaggac	614
Qy	1537	atgacaactcatcttcctgcgcagctttaaaggagttccttcagctccagctcagggct	1596
Db	615	atgacaactcatcttcctgcgcagctttaaaggagttccttcagctccagctcagggct	674
Qy	1597	cttcggcaaatgtagcatggcgcaacctoga	1626
Db	675	cttcggcaaatgtagcatggcgcaacctcaga	704
RESULT 11			
ID	N80299	standard; cDNA; 1139 BP.	
AC	N80299;	AC	
DT	08-OCT-1990	(first entry)	
DE	Interleukin 6.		
FW	IL-6; interleukin; cancer; ss.		
Key	Location/Qualifiers		
FT	cds	51..689	
FT		/*tag= a	
FT	signal_peptide	51..133	/product=IL-6
FT		/*tag= b	
FT	mat_peptide	132..686	
FT		/*tag= c	
PN	WO8800206-A.		
PD	14-JAN-1988.		
PF	07-JUL-1987; U01611.		
PR	08-JUL-1986; US-883207,		
PA	(GENE-) Genetics Inst Inc.		
PI	Clark SC, Wong GG, Schendel P, McCooy J;		
DR	WPI; 88-021566/03.		
DR	P-PSDB; P80269.		
PT	Prodn. of non-glycosylated IL-6 - for use in treatment of deficiency		
PT	disorders in haematopoietic cells and in cancer therapy.		
PS	Disclosure; p; English.		
CC	The sequence is carried by pCSF309 in E.coli MC1061 (ATCC 67153) as an		
CC	ECORI insert. It can be excised and used to construct an expression		
CC	plasmid for prodn. of IL-6. Bacterially produced IL-6 is non-		
CC	glycosylated. It can be used against diseases caused by decreased		
CC	levels of either myeloid or lymphoid cells of the haematopoietic system		
CC	It may also be used in conjunction with other interleukin therapies or		
CC	as a hybridoma growth factor in culture medium.		
CC	See also N80300.		
SQ	Sequence	1139 BP; 361 A; 240 C; 231 G; 307 T;	
Query Match 34.7%; Score 565.2; DB 1; Length 1139;			
Best Local Similarity 99.5%; Pred. No. 1.6e-133;			
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps			
Qy	1057	ccagtaacccccagagaagattccaaagattgtagcgcgccccacacagacagacactcacc	1116
Db	135	CCAGTACCCCCAGGAGAAGATTCCAAGAGATGTAGCGCGCCCCACACAGACAGCCACTCACC	194
Qy	1117	tcttcagaacgaattgacaaacaaatttcggtatccttcgagcgtatctcagccctgaga	1176
Db	195	TC TTCAGACGAATTCACAAACAAATTCGGTACATCTCTCGACGGGAYCTCAGCCCTGAGA	254
Qy	1177	aaggagacatgtaacagagtaaacatggtgaaagcagcaagaagcagcactggcagaaaac	1236
Db	255	AAGGAGACATGTACACAGAGTACATGTGTGAACGACCAAGAGGCCTCTGGCAGAAAC	314
Qy	1237	aaoctgaaccttccaaagatggctgaaaaagatggatgcttccaatctggattcaatgag	1296
Db	315	AACTGAACCTTCCAAGATGGCTGAAAAGATGATGCTTCCAATCTGGATTCAATGAG	374

```

QY 1297 gagacttcgctgggaaatacatcactcgtgtcttttggagtttgaggtatcacctagatgac 1356
D 1297 gagacttcgctgggaaatacatcactcgtgtcttttggagtttgaggtatcacctagatgac 1356
D 375 GAGACTTCGCTGGTGAAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 434
QY 1357 ctccagaacagatttgagagtagtgaggaacacccagagctgtgcagatgagtagacaaa 1416
D 1357 ctccagaacagatttgagagtagtgaggaacacccagagctgtgcagatgagtagacaaa 1416
D 435 CTCCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 494
QY 1417 gtctgatccagttcctgcagaaaaggcaagaatctagatgcaataaacaccctcgac 1476
D 1417 gtctgatccagttcctgcagaaaaggcaagaatctagatgcaataaacaccctcgac 1476
D 495 GTCTGTGATCCAGTTCTCTGCAGAAAAGCAAGAAATCTAGATGCAATAAACCCCTGAC 554
QY 1477 ccaaccacaaatgccagcctgtgcagaaagctgcagggcagcaaacacccagtgctgacgag 1536
D 1477 ccaaccacaaatgccagcctgtgcagaaagctgcagggcagcaaacacccagtgctgacgag 1536
D 555 CCAACCACAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCACTGCTGCAGGAC 614
QY 1537 atgacaactatctcattctgcagagctttaaggagttcctgcagctcagcctcagggct 1596
D 1537 atgacaactatctcattctgcagagctttaaggagttcctgcagctcagcctcagggct 1596
D 615 ATGACAACCTCATCTCAATCTCGGCAGCTTTAAGGAGTTCTTGCAGTCCAGCTCAGGGCT 674
QY 1597 ctccgcaaatgtagcctggcgcacccctcga 1626
D 1597 ctccgcaaatgtagcctggcgcacccctcga 1626
D 675 CTTCGGCAATGTAGCATGGGCACCTCAGA 704

RESULT 12
Q01763
ID Q01763 standard; DNA; 1162 BP.
AC Q01763;
DT 27-JUL-1990 (first entry)
DE BSF-2 gene for human B-cell differentiation factor.
KW BSF-2; dhfr; dihydrofolic acid reductase; differentiation.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_feature 1..708
FT cds /*tag= a
FT J02009388-A.
PN 12-JAN-1990.
PD 8-JUL-1988; 170142.
PF 9-MAR-1988; JP-055270.
PR (AJIN) Ajinomoto KK.
PA WPI; 90-055348/08.
DR P-PSDB; R05415.
DE Physiologically active protein prepn.
PT by transforming plasmid having gene coding physiologically
PT active protein and gene of dihydrofolic acid reductase to hamster
PT ovary etc.
PS Example 3; Fig 6; 12pp; Japanese.
CC Gene may be expressed by transforming a dhfr negative strain of CHO cells
CC with an active BSF-2 gene and dhfr carrying vector. The BSF-2 gene is
CC a B-cell differentiating factor.
SQ Sequence 1162 BP; 359 A; 237 C; 264 G; 302 T;

Query Match 34.7%; Score 565.2; DB 1; Length 1162;
Best Local Similarity 99.5%; Pred. No. 1.6e-133;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1057 ccagtagccccaggaagattccaaagatgtagccgccccacacagacagccactcaac 1116
D 1057 ccagtagccccaggaagattccaaagatgtagccgccccacacagacagccactcaac 1116
D 157 CCAGTAGCCCCCAGGAGAAGATTCCAAAGATGTAGCGCGCCCCACACAGACGACCTCACC 216
QY 1117 tcttcagaacgaattgacaaaataatcggtacatcctgcagcggcatctcagccctgaga 1176
D 1117 tcttcagaacgaattgacaaaataatcggtacatcctgcagcggcatctcagccctgaga 1176
D 217 TCTTCAGAACGAATTGACAAACAAATTCGGTATCTCTCGACGCGCATCTCAGCCCTGAGA 276
QY 1177 aaggagacatgtacaagagtaacatgtgtgaaagcagcaagagcagcctggcagaaaa 1236
D 1177 aaggagacatgtacaagagtaacatgtgtgaaagcagcaagagcagcctggcagaaaa 1236
D 277 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAAAGAGGCACTGGCAGAAAAC 336
QY 1237 aacctgaaccttcgaagatggctgaaaaagatggatgttccaatctgattcaatgag 1296
D 1237 aacctgaaccttcgaagatggctgaaaaagatggatgttccaatctgattcaatgag 1296

```

```

D 337 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGATGGTTCCTCAATCTGGATTCAATGAG 396
QY 1297 gagacttcgctgggaaatacatcactcgtgtcttttggagtttgaggtatcacctagatgac 1356
D 1297 gagacttcgctgggaaatacatcactcgtgtcttttggagtttgaggtatcacctagatgac 1356
D 397 GAGACTTCGCTGGTGAAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 456
QY 1357 ctccagaacagatttgagagtagtgaggaacacccagagctgtgcagatgagtagacaaa 1416
D 1357 ctccagaacagatttgagagtagtgaggaacacccagagctgtgcagatgagtagacaaa 1416
D 457 CTCCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 516
QY 1417 gtctgatccagttcctgcagaaaaggcaagaatctagatgcaataaacaccctcgac 1476
D 1417 gtctgatccagttcctgcagaaaaggcaagaatctagatgcaataaacaccctcgac 1476
D 517 GTCTGTGATCCAGTTCTCTGCAGAAAAGCAAGAAATCTAGATGCAATAAACCCCTGAC 576
QY 1477 ccaaccacaaatgccagcctgtgcagaaagctgcagggcagcaaacacccagtgctgacgag 1536
D 1477 ccaaccacaaatgccagcctgtgcagaaagctgcagggcagcaaacacccagtgctgacgag 1536
D 577 CCAACCACAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCACTGCTGCAGGAC 636
QY 1537 atgacaactatctcattctgcagagctttaaggagttcctgcagctcagcctcagggct 1596
D 1537 atgacaactatctcattctgcagagctttaaggagttcctgcagctcagcctcagggct 1596
D 637 ATGACAACCTCATCTCAATCTGGCAGCTTTAAGGAGTTCTTGCAGTCCAGCTCAGGGCT 696
QY 1597 ctccgcaaatgtagcctggcgcacccctcga 1626
D 1597 ctccgcaaatgtagcctggcgcacccctcga 1626
D 697 CTTCGGCAATGTAGCATGGGCACCTCAGA 726

RESULT 13
N90131
ID N90131 standard; DNA; 1101 BP.
AC N90131;
DT 1-NOV-1989 (first entry)
DE DNA sequence of pBSF2-L8
KW pBSF2-L8; pGEM4; cDNA; clone; Fc epsilon R-gene; IgE; allergy.
FH Key Location/Qualifiers
FT misc_feature 1..6
FT cds /*tag= a
FT /*tag= b
FT misc_feature 1097..1101
FT /*tag= c
PN EP-321842-A.
PD 28-JUN-1989; 120878.
PF 14-DEC-1988; EP-100814.
PR 22-DEC-1987; EP-100814.
PA (OSAU) Osaka University.
PI Kishimoto T, Suemura M, Kikutani H, Barsumian EL, Schneider FJ;
DR WPI; 89-186249/26.
DE P-PSDB; P90047.
PT Cloned gene for eukaryotic expression of Fc epsilon receptor
PT - for use in treatment and prophylaxis of allergy, resp. asthma.
PS Disclosure; fig 3; 24pp; English.
CC pBSF2-L8 is prep'd. by digesting pBSF-2.38 with HindIII and BamHI
CC to obtain a 1.2 kbp EcoRI-BamHI BSF-2 cDNA insert. This was digested
CC with HinfI, end-filled, and digested with KpnI. A 100 bp
CC KpnI-HinfI fragment contg. BSF-2 leader sequence was cloned into
CC the multiple cloning site of KpnI-SmaI digested pGEM4, and one of the
CC selected clones named as pBSF2-L8. It is used in prepn. of pSFC
CC epsilon R-1 (see N90132). The misc. feature a is a KpnI site, and
CC c is a BamHI site. The encoded peptide sequence (see P90047) includes
CC that of the BSF-2 signal sequence.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 34.6%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 4e-133;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1057 ccagtagccccaggaagattccaaagatgtagccgccccacacagacagccactcaac 1116
D 1057 ccagtagccccaggaagattccaaagatgtagccgccccacacagacagccactcaac 1116
D 91 CCAGTAGCCCCCAGGAGAAGATTCCAAAGATGTAGCGCGCCCCACACAGACGACCTCACC 150
QY 1117 tcttcagaacgaattgacaaaataatcggtacatcctgcagcggcatctcagccctgaga 1176

```

```
Db 151 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGACGGCATCTCAGCCCTGAGA 210
QY 1177 aaggagacatgttaacagagtaacatgtgtgaaagcagacaaagcagcactggcagaaaac 1236
Db 211 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGACAAAGAGGCACCTGGCAGAAAAAC 270
QY 1237 aacctgaaccttccaaagatggctgaaaaagatggatgcttccaatctggattcaatgag 1296
Db 271 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAAATCTGGATTCAATGAG 330
QY 1297 gagaactgctgggtgaaatcatcactggtctcttttggagtttgaggtatataccttagagtag 1356
Db 331 GAGACTTGGCTGGTGAATAATCATCACTGGTCTCTTTGGAGTTTGAGGTATACCTTAGAGTAG 390
QY 1357 ctccagaacagattgagagtagtgaggaacagcagagctgtgcagatgaatgaacaaaa 1416
Db 391 CTCACAGACAGATTTGAGAGTAGTAGGAGAACAGCCAGAGCTGTGCAGATGAGTACAAAA 450
QY 1417 gtctgtatccagtctcgcagaaaaaggcaagaatctagatgcaataaacacccctgac 1476
Db 451 GTCTGTATCCAGTTCCTGCAGAAAAAGGCAAGAAATCTAGATGCAATAACCAACCCCTGAC 510
QY 1477 caaacacaaaatgcagcctgtgcagaaagctgcagggcacagaaccagtggtgcaggag 1536
Db 511 CCAACACACAAATGCCAGCCTGCTGACGAAGCTGCAGGCGACAGAACCAAGTGGCTGCAGGAC 570
QY 1537 atgacaactcatctattctgcgcagctttaaggagttcctcagtcagccagcctgagggct 1596
Db 571 ATGACAACTCACTCAATCTGCCACGCTTTAAGGAGTTCCTGCAAGTTCAGCCCTGAGGGCT 630
QY 1597 ctgcggcaaatgtagcatgggcaccgtcga 1626
Db 631 CTTCCGCAAAATGTAGCATGGGCACCTCAGA 660

RESULT 14
N90135
ID N90135 standard; DNA; 1101 BP.
AC N90135;
DT 1-NOV-1989 (first entry)
DE DNA sequence of pBSF2-L8
KW Fc epsilon receptor; cloned gene; IgE; pBSF2-L8; allergy; asthma; BSF-2.
FH Key Location/Qualifiers
FT misc_feature 2..5
FT cds /*tag= a
FT /*tag= b
FT misc_feature 1097..1101
FT /*tag= c
EP-321601-A.
PN 28-JUN-1989.
PD 28-DEC-1987; 119080.
PR 22-DEC-1987; EP-119080.
PA (OSAU) Osaka University
PI Kishimoto T, Suemura M, Kikutani H, Barsumian E;
DR WPI; 89-186101/26.
DR P-PSDB; P90371.
PT Cloned genes coding for soluble IgE receptor - comprising modified coding
PS Sequence of Fc epsilon receptor gene.
PS Disclosure; fig. 3; 20pp; English.
CC Sequence of pBSF2-L8, which is used as a vector in prepn. of plasmid
CC pFc epsilon R-1. It is prepd. by inserting BSF-2 cDNA insert (from
CC BSF-2.38) into pGEM4. Misc. feature a is a KpnI site, and c is a BamHI
CC site. See also N90134, N90136 and P90371 for encoded peptide.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 34.6%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 4e-133;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1057 ccagtagccccaggagaagaattccaaagatgtagcgcgccccacagacagaccactcacc 1116
```

```
Db 91 CCAGTACCCCCAGGAGAAAGATTCCAAAGATGTAGCCGCCACACAGACGCCACTCACC 150
QY 1117 tcttcgagaagaattgacaaaataattcggtaacatctctcagcggcactctcagccctgaga 1176
Db 151 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGACGGCATCTCAGCCCTGAGA 210
QY 1177 aaggagacatgttaacagagtaacatgtgtgaaagcagacaaagcagcactggcagaaaac 1236
Db 211 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGACAAAGAGGCACCTGGCAGAAAAAC 270
QY 1237 aacctgaaccttccaaagatggctgaaaaagatggatgcttccaatctggattcaatgag 1296
Db 271 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAAATCTGGATTCAATGAG 330
QY 1297 gagaactgctgggtgaaatcatcactggtctcttttggagtttgaggtatataccttagagtag 1356
Db 331 GAGACTTGGCTGGTGAATAATCATCACTGGTCTCTTTGGAGTTTGAGGTATACCTTAGAGTAG 390
QY 1357 ctccagaacagattgagagtagtgaggaacagcagagctgtgcagatgaatgaacaaaa 1416
Db 391 CTCACAGACAGATTTGAGAGTAGTAGGAGAACAGCCAGAGCTGTGCAGATGAGTACAAAA 450
QY 1417 gtctgtatccagtctcgcagaaaaaggcaagaatctagatgcaataaacacccctgac 1476
Db 451 GTCTGTATCCAGTTCCTGCAGAAAAAGGCAAGAAATCTAGATGCAATAACCAACCCCTGAC 510
QY 1477 caaacacaaaatgcagcctgtgcagaaagctgcagggcacagaaccagtggtgcaggag 1536
Db 511 CCAACACACAAATGCCAGCCTGCTGACGAAGCTGCAGGCGACAGAACCAAGTGGCTGCAGGAC 570
QY 1537 atgacaactcatctattctgcgcagctttaaggagttcctcagtcagccagcctgagggct 1596
Db 571 ATGACAACTCACTCAATCTGCCACGCTTTAAGGAGTTCCTGCAAGTTCAGCCCTGAGGGCT 630
QY 1597 ctgcggcaaatgtagcatgggcaccgtcga 1626
Db 631 CTTCCGCAAAATGTAGCATGGGCACCTCAGA 660

RESULT 15
N90345
ID N90345 standard; DNA; 1101 BP.
AC N90345;
DT 1-NOV-1989 (first entry)
DE Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
DE for immunoglobulin
KW Human lymphocyte receptor for immunoglobulin; cDNA;
KW eukaryotic signal sequence; hypersensitivity; allergy; asthma;
KW BSF-2 leader sequence; plasmid pFc-epsilon-R-1; immunoglobulin E.
OS Homo sapiens (Human)
FH Key Location/Qualifiers
FT cds 7..642
FT /*tag= a
EP-324879-A.
PN 26-JUL-1989.
PD 20-JAN-1988; 100814.
PR 20-JAN-1988; EP-100814.
PA (KISH) Kishimoto T.
PI Schwenckenwein R, Sommergruber W, Swetly P;
DR WPI; 89-214148/30.
DR P-PSDB; P90121.
PT Soluble recombinant Fc-epsilon receptor
PT - used for treatment or prophylaxis of local and
PT allergic reactions induced by IgE.
PS Disclosure; fig 3; 24pp; English.
CC Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
CC for immunoglobulin (see p90121). Has BSF-2 leader sequence
CC (c.f. N90344). Used to produce highly bioactive
CC water-soluble FcR. Pref. has interleukin signal sequence.
CC Water-soluble FcR binds IgE, so it is useful for treating
CC hypersensitivity, esp. asthma.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;
```

Query Match		34.6%	Score 563.6;	DB 1;	Length 1101;
Best Local Similarity		99.3%	Pred. No. 4e-133;		
Matches 566;		Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1057	ccagtacccccagagagattccaaagatgtagcccccacacacagacagccactcacc	1116		
DB	91	CCAGTACCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACAGACGCCACTCACC	150		
QY	1117	tcttcagaacgaattgacaaataatcggtacatcctcagcgcatctcagccctgaga	1176		
DB	151	TCTTCAGAACGAATGCAAAACAAATTCCGGTACATCTCGACGGCACTCTCAGCCCTCAGA	210		
QY	1177	aaggagacatgtaacaagagtaacatgtgtgaagcagcaaaagaggcactggcagaaaaac	1236		
DB	211	AAGGAGACATGTACACAGAGTAACATGTGTGAAGCAGCAAAAGAGGCAC TGGCAGAAAAAC	270		
QY	1237	aacctgaaccttccaaagatggctgaaagagatggatgcttccaaatctggattcattgag	1296		
DB	271	AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAAATCTGGATTCAATGAG	330		
QY	1297	gagacttccttggtgaaataatcatcactgtctcttttgaggtttgaggtataccttagagtac	1356		
DB	331	GAGACTTGCTGCTGGTGAAAAATCATCACTGCTCTTTTGGAGTTTGAGGTATACCTAGAGTAC	390		
QY	1357	ctccagacacagatttgagagtagtgaggaacaagccagagctgtgcagatgaggtacaaaa	1416		
DB	391	CTCCAGAACAGATTTCAGAGTAGTCAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA	450		
QY	1417	gtcctgatacagttcctgcagaaaaagcaagaatactagatgcaataaccacccctgac	1476		
DB	451	GTCCCTGATCCAGTTCTCTGCAGAAAAGGCAAGAATCTAGATGCAATAACCCCTCGAC	510		
QY	1477	ccaaccacaaatgccagcctgtgcagagctgcagggcacagaaaccagtggtgcaggac	1536		
DB	511	CCAACCACAAAATGCCAGCTGCTGACGAGCTGCAGGCACAGAACCACTGGCTGCAGGAC	570		
QY	1537	atgacaactcatctcattctgcgcagcctttaaggaggttcctgcagtcagcctgagggct	1596		
DB	571	ATGACAACCTCATCTCTTCTGGCGACGCTTAAAGGAGTTCTCTGCAGTTCAGCCTGAGGGCT	630		
QY	1597	cttcggcaaatgtagcatggccacgtcga	1626		
DB	631	CTTCGGCAAAATGTAGCATGGGCACCTCAGA	660		

Search completed: August 9, 2000, 09:34:22
Job time: 34128 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2000, 13:48:06 ; Search time 2865.12 Seconds
(without alignments)
1013.466 Million cell updates/sec

Title: US-09-142-471-1
Perfect score: 1627
Sequence: 1 gtcacatgagtgtag.....gtacatgggcaacgtcgac 1627

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues 1945680
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pl3.*
10: gb_pr2.*
11: gb_pr3.*
12: gb_ro.*
13: gb_sts.*
14: gb_sy.*
15: gb_un.*
16: em_fun.*
17: em_hum1.*
18: em_hum2.*
19: em_in.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_sy.*
29: em_un.*
30: em_v1.*
31: gb_htg1.*
32: gb_htg2.*
33: gb_in1.*
34: gb_in2.*
35: em_ba1.*
36: em_ba2.*
37: em_hum3.*
38: em_hum4.*
39: gb_pr4.*
40: gb_htg3.*
41: gb_htg4.*
42: gb_htg5.*
43: gb_htg6.*

44: gb_htg7.*
45: em_htg1.*
46: em_htg2.*
47: em_htg3.*
48: em_hum5.*
49: gb_pl3.*
50: gb_pr5.*
51: gb_htg8.*
52: gb_htg9.*
53: gb_htg10.*
54: gb_htg11.*
55: gb_htg12.*
56: gb_htg13.*
57: gb_htg14.*
58: gb_in3.*
59: gb_htg15.*
60: gb_htg16.*
61: gb_htg17.*
62: em_htg4.*
63: em_htg5.*
64: em_htg6.*
65: em_htg7.*
66: em_hum6.*
67: gb_htg18.*
68: gb_htg19.*
69: gb_htg20.*
70: gb_htg21.*
71: gb_htg22.*
72: gb_htg23.*
73: gb_htg24.*
74: gb_htg25.*
75: gb_htg26.*
76: gb_htg27.*
77: gb_htg28.*
78: gb_htg29.*
79: gb_htg30.*
80: gb_htg31.*
81: gb_vil.*
82: gb_vil2.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1627	100.0	1627	5	A93714	A93714 Sequence 1
2	1587	97.5	1612	5	A93715	A93715 Sequence 2
3	995	61.2	2066	5	E04823	E04823 CDNA encodi
4	995	61.2	2087	5	E02673	E02673 CDNA encodi
5	995	61.2	3319	5	E12979	E12979 CDNA encodi
6	995	61.2	3319	9	HSIL6R	X12830 Human mRNA
7	993.4	61.1	1486	9	HSIL6RC	X58298 Human mRNA
8	969	59.6	1074	5	AR031384	AR031384 Sequence
C 9	581	35.7	167677	69	AC013588	AC013588 Homo sapi
C 10	581	35.7	175587	59	AC015889	AC015889 Homo sapi
C 11	577.8	35.5	168014	40	AL353649	AL353649 Homo sapi
12	577.8	35.5	168372	40	AL161629	AL161629 Homo sapi
13	565.2	34.7	1098	9	HSILB2R	X04602 Human mRNA
14	565.2	34.7	1102	5	E03737	E03737 CDNA encodi
15	565.2	34.7	1102	10	HUMIL6C	M29150 Human inter
16	565.2	34.7	1113	11	HUMIL6CSF	M54894 Human inter
17	565.2	34.7	1125	9	HUMIFNB2B	M18403 Human hybri
18	565.2	34.7	1139	5	I08633	I08633 Sequence 2
19	565.2	34.7	1161	5	E01616	E01616 CDNA encodi
20	565.2	34.7	1162	5	E01518	E01518 DNA encodin
21	565.2	34.7	1162	5	E01537	E01537 DNA encodin
22	565.2	34.7	1162	5	E02030	E02030 CDNA sequen
23	565.2	34.7	1162	5	E02202	E02202 DNA encodin
24	565.2	34.7	1162	5	E02930	E02930 DNA sequenc

Thu Aug 10 17:14:03 2000

	25	565.2	34.7	1162	23	EL1969	EL1969 CDNA encod1
26	563.6	34.6	1101	5	A10873	A10873 pBSF2-L8 DN	
27	563.6	34.6	1101	5	A11845	A11845 Nucleotide	
28	563.6	34.6	1101	5	A13367	A13367 pBSF2-L8 DN	
29	563.6	34.6	1101	5	A13486	A13486 pBSF2-L8 DN	
30	563.6	34.6	1101	5	A14652	A14652 pBSF2-L8. 3	
31	563.6	34.6	1128	9	HUMINB2	M14584 Human inter	
32	563.6	34.6	1145	9	A09363	A09363 H.sapiens m	
33	563.6	34.6	1145	9	HSIFINB2R	X04430 Human IFN-b	
34	558	34.3	657	39	S56892	S56892 interleukin	
35	556.2	34.2	970	9	HS26KRDAR	X04403 Human mRNA	
36	552.2	33.9	566	5	I08634	I08634 Sequence 4	
37	551.8	33.9	555	5	A38783	A38783 Sequence 1	
38	551.8	33.9	555	5	I71331	I71331 Sequence 1	
39	550.4	33.8	561	5	I52043	I52043 Sequence 19	
40	549	33.7	560	5	E02170	E02170 Human B cel	
41	547.2	33.6	555	5	E02172	E02172 Human B cel	
42	545.6	33.5	555	5	E02205	E02205 DNA encodin	
43	545.2	33.5	683	9	AB000554	AB000554 Macaca fa	
44	541.8	33.3	2854	9	HS3IL6R	X79982 H.sapiens S	
45	541	33.3	663	5	A93806	A93806 Sequence 1	

ALIGNMENTS

RESULT	1
A93714	
LOCUS	1627 bp DNA
DEFINITION	Sequence 1 from Patent WO9732891.
ACCESSION	A93714
VERSION	A93714.1 GI:6741885
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unidentified
REFERENCE	1 (bases 1 to 1627)
AUTHORS	Rose-John,S.
TITLE	CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
JOURNAL	PATENT: WO 9732891-A 12-SEP-1997;
FEATURES	ANGEWANDTE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE) source Location/Qualifiers 1..1627 /organism="unidentified" /db_xref="taxon:32644" 34..90 34..1611 sig_peptide CDS /note="unnamed protein product" /codon_start=1 /protein_id="CAB69604.1" /db_xref="GI:6741886" /translation="MLAVGCALLALIAAPLAPRCPAQVARGVLTSPLSDSVT LTCPGEPEPDNAYHVHLRKPAGSHPSWAGMRLLRSVOLHDSGNVSCYGRAP AGTVHLLVDVPPEQLSCPFRKPLSNVCWEFGPRSTPSTTKAYLLVRKFQNSPAD FPQCYSQSBSFCSQLAPEGDSFYIVSMCVASSVGSKFTKTQTFFCGGLIQDP PANITYTAVARNRWLSVTWQDFHSWNSSFYRLRYELRYRAERSKTFITVMWKDLQH CVITHDAMSGLRHVWLQAQFECSGWSESPAMGTPTWTESRSPARGGGGGGGGS GGGSEVEYPGDSKDVAAPHQPLTSSERIDQIRYLIDGISALKRKETCNKSNNCE SSKEALEANNLNLPKNAEKDCGFSGNFNETCLVKIITGLEFEVLEYLQNRFESSE EQARVQMSTKVLIQIFLOKKAKNLDAITPDPDTNASLLTLKLQAQNWQLDMTHLLL RSKFEFLQSSRALRQM"
BASE COUNT	388 a 450 c 308 t
ORIGIN	mat_peptide 91..1608

	Query Match	100.0%;	Score 1627;	DB 5;	Length 1627;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1627;	Conservative	0;	Mismatches	0; Indels
					Gaps
					0;
Oy	1	gtcacgcgatgagtggtgacgcgaggaggagacatgctggcctgcgctgcgctgctg	60		
pb	1	gtcacgcgatgagtggtgacgcgaggaggagacatgctggcctgcgctgcgctgctg	60		

QY 1141 attcgatcatctcgacggcatctcagccctgagaaaggagacatgttaacaagatgaac 1200
DB 1141 ATTCGGTACATCTCGACGGCATCTCAGCCCTGAGAAAGGAGACATGTAACAGACTAAC 1200
QY 1201 atgtgtgaagcagcaaaaggagcactggcagaaaaaaccttgaaccttccaagatggct 1260
DB 1201 ATGTGTGAAGCAGCAAAAGGACACTGGCAGAAAAACAACCTGAACCTTCCAAGATGGCT 1260
QY 1261 gaaaaagatggatgcttccaattctgattcaatgagagagacttgcctggtgaaaaatcatc 1320
DB 1261 GAAAAAGATGGATGCTTCACATCTGATTCATATGAGAGACTTGCCTGGTGAATAATCATC 1320
QY 1321 actggtcttttggagtttgaggtatatacctagatagactccagaacagattgagagtagt 1380
DB 1321 ACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTACCTCCAGAACAGATTTGAGAGTAGT 1380
QY 1381 gaggaaacagcagagacttgagatgagtacaaaaagtcctgatccagttcctctgcagaaa 1440
DB 1381 GAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAAAGTCTGTATCCAGTTCTCTGCAGAAA 1440
QY 1441 aaggcacaagaatctagatgaataaacccctgaccccaaccacaaaatgccagcctgctg 1500
DB 1441 AAGGCAAGAAATCTAGATGCATATACCAACCCCTGACCCCAACCAAAATGCCAGCCTGCTG 1500
QY 1501 acgaagctcaggacacagacagtggtgcaggagacatgacaaactcatctcttctgcgc 1560
DB 1501 ACGAAGCTCAGGCACAGAACAGTGGCTGCAGGACATGACAATCATCTCATCTTCGCGC 1560
QY 1561 agctttaagagttcctgcagtcagctcagcctgagggctctctcgcaaatgtagcatgggac 1620
DB 1561 AGCTTTAAGAGTTCTCGAGTCCAGCCTGAGGGCTCTTTCCGCAAAATGATGATGGGCAC 1620
QY 1621 cgtcgac 1627
DB 1621 CGTCGAC 1627

RESULT 2
LOCUS A93715 1612 bp DNA PAT 22-JAN-2000
DEFINITION Sequence 2 from Patent WO9732891.
ACCESSION A93715
VERSION A93715.1 GI:6741887
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1612)
AUTHORS Rose-John,S.
TITLE CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
JOURNAL Patent: WO 9732891-A 12-SEP-1997;
ANGEWANDTE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
FEATURES
source
1. .1612
/organism="unidentified"
/db_xref="taxon:32644"
sig_peptide
34. .90
CDS
/note="unnamed protein product"
/codon_start=1
/db_xref="GI:6741888"
/translation="MLAVGCLALLAALPAAGLAAPRCPAQEVARGVLTSLPGDSVT
LTCGVEPEDNATVHWLRKPAGSHPSRWAGMGRLLRLRSVLQHDNSGYRAGR
ACTVHLLVDVPEEPQLSCFRKPSLNVCWEWPRSTSLTKAVLLVRKQNSPAED
FQEPQYSDSESOKFSQLAVPEGDSFYSIVMSVASSVSKFSKTQTQGGCIIQDP
PANITVAVARNRWLSVETWQDPHSWNSFYLRLRFLRYRAERSPTFTTWMVKDLQHH
CVIHDWGLRHVQLRAQEFQGWSEWSPFAMTPTWERSPPARGGSGGGGS
VEVPPEGDSKDVAAHPROPLTSSERIDKQIRYILDGI SALRKETCNKSNMCESSKEA
LAEMNLPLFKPAEKDGCQFQSGFNSETCLVKITGLLBEVLEYILEYLNRFSESEQARA
VQSSLRALQM"
91. .1593

mat_peptide

BASE COUNT 386 a 449 c 473 g 304 t
ORIGIN
Query Match 97.5%; Score 1587; DB 5; Length 1612;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1612; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
QY 1 gtcgacgatgagtgtagccgaggaaggaagcagctggtccgtcggtcggtcggtcg 60
DB 1 GTCGACGATGAGTGGTAGCCGAGGAGGAGCATGCTGGCCGTCGGCTCGCGCTGCTG 60
QY 61 gctgcctctgctgcccgcgcgggagcgctggcccaaggcgctggcccaaggcgctgcgcaagg 120
DB 61 GCTGCCCTGCTGCCCGCGCGGGAGCGCGCTGCCCCCAAGCGCTGCCCTGGCAGGAG 120
QY 121 gtggcaagggcgtgctgaccagctctgccaggagagcagcgtgactctgacctgcccgggg 180
DB 121 GTGGCAAGAGGCGTGTGCTGACAGCTCTGCCAGGAGACAGCGTGACTCTGACTTGCCTG 180
QY 181 gttagccggaagacaatccactgttccactgttccactgttccactgttccactgttccactgt 240
DB 181 GTAGACCCGGAAGACAATGCCACTGTTCCTGGGTGCTCAGGAAGCGCGCTGCAGGCTCC 240
QY 241 caccacagcagatgggctggcagtggaaggagcgtgctgctgaggtcggtgaggtcggtgaggtcg 300
DB 241 CACCCACAGCAGATGGCGTGGCATGGGAGGAGGCTGCTGCTGAGTCTGGTGCAGTCCAC 300
QY 301 gactctggaaactattcatctgctaccggcgccggccagcgtgggactgtgcaacttgcgtg 360
DB 301 GACTCTGGAAACTATTTCATGCTTACCGGGCGCGCGCCAGCTGGGACTGTGTGCATCTGCTG 360
QY 361 gtggatgttccccccgagagagcccgactctctctctcgttcggaagagcccccacacaat 420
DB 361 GTGGATGTTCCCCCGAGGAGGAGCCCGAGCTCTCTGCTTCCGGAAGAGCGCCCCCTCAGCAAT 420
QY 421 gttgttgtgagtggggtctcctcgagacacccccatccccctgcagacaaaggcgtgtgctctg 480
DB 421 GTTGTGTTGTGAGTGGGTCTCTCGAGACACCCCATCCTGTAGCAGACAAAGGCTGTGCTCTTG 480
QY 481 gtggaagatttcagaaacagtcgcggcggaagacttccaggagccgtgcaagtattccag 540
DB 481 GTGAGGAAGTTTCAGAACAGTCCGCGCGCAAGACTTCCAGGAGCGCGTCCCAAGTATTCCAC 540
QY 541 gagtcccaagaagtctcctgcagttagcgtcccgagaggaaggaagacagctcttctacata 600
DB 541 GAGTCCCAAGAAGTCTCTCTGCCAGTTAGCAGTCCCGGAGGAGAGACAGCTCTTTTACATA 600
QY 601 gtgtccatgtgcgtcgccagtagtgcgggagcaagtccagcaaaactcaaacctttcag 660
DB 601 GTGTCCATGTGCGTCCGCGCAGTAGTGTGCGGAGCAAGTTCAGCAAAACTCAAACTTTCAG 660
QY 661 ggtgtggaattctgagcctgatccgcctgcgaacatcagtcactgcctggtggcaga 720
DB 661 GGTGTGGAATCTTGACGCGCTGATCGCGCTGCCAATCATCAGTCACTGCTGCGTGGCAGA 720
QY 721 aacccccgctggtcagtgctacactggcaagacccccactcctggaactcatattttac 780
DB 721 AACCCCCGTGGCTCAGTGTACCTGGCAAGACCCCACTCTCTGGAACACTCATCTTTCTAC 780
QY 781 agactcgggtttgagctcagatcagggtggaacggtggaacggtggaacggtggaacggtggaacg 840
DB 781 AGACTACGGTTTGAGCTCAGATATCGGGCTGAACGGTCAAGAGCATTCACAACATGGATG 840
QY 841 gtaaggaacctccagcatacactgtgtatccacagcgtcggtgagcggtcggtgagcggtg 900
DB 841 GTCAAGGACCTCCAGCATCACTGTGTATCCAGACGCGCTTGAGCGCGCTTGAGCGCAGGTG 900
QY 901 gtgcagcttcgtgccagagaggttcggaagagaggtgcggcaagagaggtgcgagtagtgagcgccgag 960
DB 901 GTGCAGCTTCGTGCCAGGAGGAGTTCGGCAAGGCGGAGTGGAGCGGAGTGGAGCGCGGAG 960
QY 961 gccatgggcacgccttggacagaatccaggagtcctccagcgtcagaggaggtgaggttct 1020

Db	961	GCCATGGCAGCGCTTGACAGAAATCCAGAGTCTCCAGCTCGA-----	1005
Qy	1021	ggaggtgaggttctcgaggtggaggttctgagccagtagcccccagagattcc	1080
Db	1006	GGAGGTGAGGTTCTGGAGGTGAGGTTCTGTCGAGCCAGTACCCCCAGGAGATTC	1065
Qy	1081	aaagatgtagccgccccacacagacagccactccttcagaacgaattgacaaaca	1140
Db	1066	AAAGATGTAGCGCCGCCACACAGACAGCCACTACCTCTTTCAGAACGAATTCACAA	1125
Qy	1141	attcggtacatcttcgagcggtatcagccctgagaagagacatgtaacaagagtaac	1200
Db	1126	ATTCGGTACATCTCGACGGCTCTCAGCCCTGAGAAGAGACATGTACACAGATTAAC	1185
Qy	1201	atgtgtgaaagcagcaaaagagcactggcagaacacactgaaccttccaaagatggtc	1260
Db	1186	ATGTGTGAAAGCAGCAAAAGAGCAGCTGGCAGAAAACAACTGAACCTTCCAAAGATGGCT	1245
Qy	1261	gaaaagatgtagcttccaatctggtattcaatgaggagacttccctggtgaaatcatc	1320
Db	1246	GAAAAGATGATGCTTCCAACTCTGGAATCAATGAGGAGACTTGCCTGGTGAATAATCATC	1305
Qy	1321	actggtcttttggagttgaggtatactagatgacctccagaacagatttgagagtagt	1380
Db	1306	ACTGTCTTTTGGAGTTTGAGGTATACCTAGAGTACCTCCAGACAGATTTGACAGTAGT	1365
Qy	1381	gaggacaagccagagctgtgcagatgagtacaaaagtcctgattccctgcagaaa	1440
Db	1366	GAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAAGTCTCTGATCCAGTTCCTGCAGAAA	1425
Qy	1441	aaggcaagaatctagatgcaataacacccctgacccaacacaaatgcccagctctg	1500
Db	1426	AAGGCAAGAATCTAGATGCAATAACCAACCCCTGACCAACCAAAATGCCAGCTGTCTG	1485
Qy	1501	acgaagctgcagcagacagaacagtggtgcaggagcatgacaactcatcttctgcgc	1560
Db	1486	ACGAAGCTGCAGCAGACAGACAGTGGCTGCAGGACATGACAATCATCTATTCTGGCG	1545
Qy	1561	agctttaaggagttcctgcagtcacgctgagggctcttcggcaaatgtagctgggac	1620
Db	1546	AGCTTTAAGGAGTTCTGTCAGTCCAGCTCCAGGGCTCTTCGGCAAAATGATGATGGGCAC	1605
Qy	1621	cgtcagac	1627
Db	1606	CGTCGAC	1612
RESULT	3		
E04823			
LOCUS	E04823	2066 bp	RNA PAT 29-SEP-1997
DEFINITION	CDNA encoding interleukin 6 receptor.		
ACCESSION	E04823		
VERSION	E04823.1	GI:2173019	
KEYWORDS	JP 1993091892-A/1.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
AUTHORS	Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 2066)		
JOURNAL	Kishimoto,C., Hachiman,H. and Yasukawa,K. .		
COMMENT	IL-6 RECEPTOR DERIVATIVE		
	Patent: JP 1993091892-A 1 16-APR-1993;		
	KISHIMOTO CHUZO, CHUGAI PHARMACEUT CO LTD, TOSOH CORP		
	OS Homo sapiens (human)		
	PN JP 1993091892-A/1		
	PD 16-APR-1993		
	PF 02-OCT-1991 JP 1991255521		
	PI KISHIMOTO CHUZO, HACHIMAN HIDEO, YASUKAWA KIYOSHI PC		
	C12P21/02,C07K13/00,C12N5/10,C12N15/12,(C12P21/02,C12R1:91); CC		
	strandedness: Double;		
	CC topology: Linear;		
	CC hypothetical: No;		

CC	anti-sense: No;	Location/Qualifiers	
PH	Key		
PH	5'UTR	1..225	
FT	CDS	226..1632	
FT		/product='interleukin 6 receptor' FT	3'UTR
		1633..2066.	
FEATURES	Location/Qualifiers		
source	1..2066		
	/organism='Homo sapiens'		
	/db_xref='taxon:9606'		
BASE COUNT	420 a	642 c	615 g
ORIGIN			389 t
Query Match 61.2%; Score 995; DB 5: Length 2066;			
Best Local Similarity 100.0%; Pred. No. 3.6e-225;			
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	8	catggagtgtagccgagggagagcatgctggccgtcgcgctgcgctgctggtgctgccc	67
Db	200	CATGGAGTGTGTAGCCGAGGAGGAGCATGCTGGCCGTGCGCTGCGCTGCTGGCTGCC	259
Qy	68	tgtgtgcccgcgcccggagcggtgctggcccaaggcgctgcccctgcgcagagagtgga	127
Db	260	TGCTTGGCCGCGCGGAGCGGCTGGCCCCAAAGCGCTGCCCTGCGCAGGAGGTGGCA	319
Qy	128	gagggctgtgacagctctccagagagacgctgactgacctgacctgcccggggtagagc	187
Db	320	GAGGCGTGTGACCACTGCTGCCAGGAGACAGCTGACTCTGACCTGCCCGGGGTAGAGC	379
Qy	188	cgaagaacaatgccactgttcaactgggtgcaggaagccggctcaggtcccaaccca	247
Db	380	CGGAAGACAAATGCCACTGTTCACTGGGTGCTCAGGAAGCGGCTGCAGGCTCCACCCCA	439
Qy	248	gcagatgggtggtgcatgggaaggaggtgctgtgaggtcgggtgcagctccagactctg	307
Db	440	GCAGATGGGTGGCATGGGAAGAGGCTGCTGTGAGTGGTGCAGCTCCAGACTCTG	499
Qy	308	gaaactattcatgctacgcggcgccgcagctgggactgtgacctgtgctggtgagtg	367
Db	500	GAAACTATTATGCTACCGGGCGCGCCAGCTGGGACTGTGCACTTGTGTGGTGGATG	559
Qy	368	ttcccccgagggagcccccagctctcctgcgcgagagagcccccctcagaaattgtttt	427
Db	560	TTCCCCCGAGGAGCGCCAGCTCTCTCTCTCCGGAAGAGCGCCCTCAGCAATGTTGTT	619
Qy	428	gtgagtggtggtctcgcagagacacccatccctgcgcgacaaaggctgtgctcttggtagga	487
Db	620	GTGAGTGGGGTCTCTCGGAGACACCCCATCCCTGACGACAAAGGCTGTGCTCTTGTGAGGA	679
Qy	488	agtttcagaaacagtcgccgcccgaagacttccaggagccggtgcagattatcccaaggagtc	547
Db	680	AGTTTCAGAACAGTCCGCGCCGAAGACTTCCAGAGAGCGGTGCAGTATTCCAGAGAGTCCC	739
Qy	548	agaagttctcctgccagttagcagtcgccgagggagacagctctttctacatagtcca	607
Db	740	AGAAATTTCTCTGTCAGTTAGTTCAGTCCCGGAGGAGACAGCTCTTCTTACATAGTGTCCA	799
Qy	608	tgtcgctgcagtagtgtcgggagcaagttcagcaaaactcaaaccttttcaggggtgtg	667
Db	800	TGTGGCTGCCAGCTAGTGTTCGGGAGCAAGTTTCAGCAAAACTCAAACCTTTTCAGGGTTGTG	859
Qy	668	gaattctgcagctgattccgctgccaacatcaacagtcactgcggtggcagaacacccc	727
Db	860	GAATCTTGCAGCCTGATCCGCTGCCAATCATCAGTCACTGCCGTGGCCAGAAACCCCC	919
Qy	728	gctggtcaggtgacactggaagacacccactcctggaactcatcttctcacagactac	787
Db	920	GCTGGCTCAGTGTACCTTGGCAAGACCCCACTCTCTGGAATCATCTTCTACAGACTAC	979
Qy	788	ggttgagctcagatattcgggtgaacggtcaagacattcacacatggtatggtcaagg	847

ACCESSION	E12979
VERSION	E12979.1 GI:3251803
KEYWORDS	JP 1997118623-A/1.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens.
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3319)
AUTHORS	Kutomaru,K. and Koishihara,Y..
TITLE	HUMAN INTERLEUKIN-6 RECEPTOR-DEVELOPING INHIBITOR
JOURNAL	Patent: JP 1997118623-A 1 06-MAY-1997;
COMMENT	CHUGAI PHARMACEUT CO LTD OS Homo sapiens (human) PN JP 1997118623-A/1 PD 06-MAY-1997 PR 12-DEC-1995 JP 1995323130 PF 16-DEC-1994 JP 94P 313167, 18-AUG-1995 JP 95P 210739 PC A61K31/70,A61K48/00,C07H21/04/C12N15/09; CC strandedness: Double; CC topology: Linear; CC hypothetical: No; CC anti-sense: No; FH Key Location/Qualifiers FH source 1..3319 FT /organism='Homo sapiens' FT /cell_line='CHO.SR344' FT 5'UTR 1..437 FT CDS 438..1844 FT product='Human interleukin-6 receptor' FT 3'UTR 1845..3319 FT misc_structure 640..685 FT /note='Loop structure' FT misc_structure 770..810 FT /note='Loop structure' FT misc_structure 1340..1375 FT /note='Loop structure' FT misc_structure 460..475 FT /note='Loop structure' FT misc_structure 535..560 FT /note='Loop structure' FT misc_structure 925..960 FT /note='Loop structure' FT misc_structure 815..840 FT /note='Loop structure'. FEATURES source Location/Qualifiers 1..3319 /organism='Homo sapiens' /db_xref='taxon:9606' BASE COUNT 735 a 935 c 962 g 687 t ORIGIN Query Match 61.2%; Score 995; DB 5; Length 3319; Best Local Similarity 100.0%; Pred.No. 3.7e-225; Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps QY 8 catggagtgttagccgaggaggaacatgcctggcctcgctgcgcgtgcgtgcgtgcgc 67 DB 412 CATGGAGTGTGATGCCGAGGAGGAGCATCTGTGCCTGCGCCTGCGCTGCGC 471 QY 68 tgctggccgcgccgggagcgcgctggcccccaaggcgctgcctgcgcaggaggtcgcaa 127 DB 472 TGCTGGCCGCCGCCGGAGCGCGCTGGCCCCCAAGAGCGCTGCCTGCAGGAGGTGGCAA 531 QY 128 gaggcgtactaacacgttgcgcaggagaacagctgacctgacctgcccggggtagagc 187 DB 532 GAGGCGTGCTGACCAGTCTGCCAGAGACAGCGTGACTCTGACCTGCCCGGGGTAGAGC 591 QY 188 cggaagacaattgccactgttcactgggtgtctcaggaagcgcgctgcaggtcccaccoca 247 592 CGGACACATTCOTACTGTTTACTTGGTGTCTCAGGAAGCGGCTGCAGGCTCCACCCCA 651

AUTHORS Yamasaki, K., Taga, T., Hirata, Y., Yawata, H., Kawanishi, Y., Seed, B.,
 Taniguchi, T., Hirano, T. and Kishimoto, T.
TITLE Cloning and expression of the human interleukin-6 (BSF-2/IFN beta
 2) receptor
JOURNAL Science 241 (4867), 825-828 (1988)
MEDLINE 88305347
FEATURES Location/Qualifiers
 1..3319
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="YF"
 /clone="pBSF2R.236"
 438..494
 /product="signal peptide (AA -19 to -1)"
 438..1844
 /codon_start=1
 /product="IL-6 receptor precursor (AA -19 to 449)"
 /protein_id="CAA31312.1"
 /db_xref="GI:33846"
 /db_xref="SWISS-PROT:P08887"
 /translation="MLAVGCALLAALLAAGPAAAPRRCPAQEVARGVLTSLPGDSVT
 LTCPEVEDNATVHWLRKPKAGSHPSRWAGMGRPLLLRSVOLHDSNGYSCYRAGR
 AGTVHLLVDVPEEPQLSCFRKSPNSVYCEWGPSTSLTKAVLLKRFQNSPAED
 FOEPCVSOESQKFCQLAVPEGDSFIVCMVASVSGSKFSKTQTGGCGILQDP
 PANITVAVARNPRLSVTWDPHSWNSFYRLRFLRYRAERSKFTTVMVKDLQHH
 CVIHDWGLRHVQLRAQEFQGESEWSEPMAGTWPTESRSPPAENEVSTPMQAL
 TTNKDDNLLFRDSANATSLPVQDSSVPLPTFLVAGGSLAFGLTLLCIAIVLRFKTW
 KLRLKEGKTSNHPYSLGQLVPERPTPLVPLISPPVSPSSLGSDNTSSHNRPDA
 RDRSPYDISNTDFFPR"
 495..1841
 /product="IL-6 receptor (AA 1-449)"
 495..764
 /note="Ig superfamily domain"
 600..608
 /note="pot. N-linked glycosylation site"
 714..722
 /note="pot. N-linked glycosylation site"
 1098..1106
 /note="pot. N-linked glycosylation site"
 1170..1178
 /note="pot. N-linked glycosylation site"
 1485..1493
 /note="pot. N-linked glycosylation site"
 1512..1595
 /note="transmembrane domain"
 1758..1766
 /note="pot. N-linked glycosylation site"
 3134..3139
 /note="pot. polyA signal"
 3159..3164
 /note="pot.alt. polyA signal"
 3319
 /note="polyA site"
 735 a 935 c 962 g 687 t
BASE COUNT
ORIGIN
 Query Match 61.2%; Score 995; DB 9; Length 3319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-225;
 Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 catgagtgtagcagcagagaagcatgtgcccgtcgctgacgcgtgctggtgccc 67
 Db 412 CATGAGTGTGAGCCAGAGAGAGCATGCTGCCGTCGGCTGCGGCTGCTGGCTGCC 471
 Qy 68 tgcgtgccgc 127
 Db 472 TCGTGGCCCGCGCGGAGCGCGCTGGCCCAAGGGCTGCCCTGGCAGGAGGTGGCAA 531
 Qy 128 gaggcgtgctgaccagtcgtccagcagacagcgtgactctgacctgccccggggtagagc 187
 Db 532 GAGCGCTGTGACCACTGTCGCCAGGAGACAGCGTACTCTGACCTGCCCGGGGTAGAGC 591

QY 188 cggaacacaatgccactgttctactgggtgtcctcaggaagccggtcaggtccacccca 247
 Db 592 CGGAACACATGCGCATGTCTACTGGTGTCTCAGGAAGCCGCTGAGGGTCCACCCCA 651
 QY 248 gcagatgggtggcattggaagagagctgctgctgaggtggtggtgcagctccagactctg 307
 Db 652 GCAGATGGGTGGCATGGGAAGGAGGCTGCTGCTGAGGTGGTGCAGTCCACGACTCTG 711
 QY 308 gaaactattcatctaccggcgccgcgcagctgggactgtgactgtggtggtggtg 367
 Db 712 GAAACTATTATGCTACCGGGCGCGCCAGCTGGGACTGTGCACTTGTCTGGTGGATG 771
 QY 368 ttccccccgag 427
 Db 772 TTCCCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 831
 QY 428 gtgagtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 487
 Db 832 GTGAGTGGGTGCTCTCGGAGCACCCTCCCTGACGACAAAGGCTGTGCTCTTGGTGAGGA 891
 QY 488 agtttcagaacagctccggcgccgagagagagagagagagagagagagagagagagag 547
 Db 892 AGTTTCAGAACAGTCCGGCGGAGAGACTTCCAGAGCGCTGCCAGTATTCACGAGGTCCC 951
 QY 548 agaagtctctccgtccagcttagcagctccggagagagagagagagagagagagagagag 607
 Db 952 AGAAGTCTCTCTGCGAGTGTAGCAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1011
 QY 608 tctgctgcccagtagtctggtggagcaagtccagcaaaactcaaaccttccaggggtgtg 667
 Db 1012 TGTGCGTCCGCGAGTGTGCGGAGCAAGTTCAGCAAACTCAAACTTTTCAGGGTGTG 1071
 QY 668 gaattctgagcctgagctccgctgcaacatcaacagctcagctggtggcagaaaccccc 727
 Db 1072 GAATCTTGACGCTGATCCGCTGCCAACATCACATGCTACTGCGTGGCCAGAAACCCCC 1131
 QY 728 gctggctcagtgctcactgtgcaagacccccactctcggaaactcatctttacagactac 787
 Db 1132 GCTGGCTCAGTGTACCTGGCAAGACCCCTCTCTGGAACATCATCTTTCTACAGACTAC 1191
 QY 788 ggttgagctcagatcctgggtggaacggtgcaaacagattcacaacatggatgggtcaag 847
 Db 1192 GGTTCAGCTCAGATATCGGCTGAACGGTCAAAAGACATTCAACATGGATGCTCAAGG 1251
 QY 848 acctcagcagctcagctgctcagcagcagcagcagcagcagcagcagcagcagcagcagc 907
 Db 1252 ACTCCAGCATCACTGTGTCATCCAGCAGCCTGGAGCGGCTGGAGCGAGCTGGTGCAGC 1311
 QY 908 ttctgtcccagagagaggttcggcagagcagcagcagcagcagcagcagcagcagcagc 967
 Db 1312 TTCTGTCCCAGGAGGAGTTCGGGCAAGCGGAGTGGAGCGGAGTGGAGCGGCGGAGCATGG 1371
 QY 968 gcacgcttgagcagaatccagagagctccctccagct 1002
 Db 1372 GCACGCTTGGACAGATCCAGGAGTCTCCAGCT 1406

RESULT 7
HSI6REC
LOCUS
DEFINITION Human mRNA for interleukin-6-receptor.
ACCESSION X58298
VERSION X58298.1 GI:32580
KEYWORDS cell surface receptor; interleukin 6 receptor.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Primates; Catarrhini; Hominidae; Homo.
TITLE I (bases 1 to 1486)
JOURNAL Schooltink, H.
 Submitted (12-MAR-1991) H. Schooltink, Dept of Biochemistry, RWTH
 Aachen Klinikum, Pauwelsstrasse 30, 5100 Aachen, Germany


```

* 21266 21365: gap of 100 bp
* 21366 28896: contig of 7531 bp in length
* 28897 28996: gap of 100 bp
* 28997 34811: contig of 5815 bp in length
* 34812 34911: gap of 100 bp
* 34912 42526: contig of 7615 bp in length
* 42527 42626: gap of 100 bp
* 42627 54970: contig of 12344 bp in length
* 54971 55070: gap of 100 bp
* 55071 65926: contig of 10856 bp in length
* 65927 66026: gap of 100 bp
* 66027 79951: contig of 13925 bp in length
* 79952 80051: gap of 100 bp
* 80052 98416: contig of 18365 bp in length
* 98417 98516: gap of 100 bp
* 98517 119303: contig of 20787 bp in length
* 119304 119403: gap of 100 bp
* 119404 167677: contig of 48274 bp in length.

```

FEATURES

```

source
1..167677
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-8B23"
/clone_lib="RPC1-11 Human Male BAC"
1..2090
/note="assembly_fragment"
2191..4992
/note="assembly_fragment"
5093..7384
/note="assembly_fragment"
7485..11034
/note="assembly_fragment"
11135..15041
/note="assembly_fragment"
clone_end:SP6
vector_side:left
15142..21265
/note="assembly_fragment"
21366..28896
/note="assembly_fragment"
clone_end:SP6
vector_side:right
28997..34811
/note="assembly_fragment"
34912..42526
/note="assembly_fragment"
42627..54970
/note="assembly_fragment"
55071..65926
/note="assembly_fragment"
66027..79951
/note="assembly_fragment"
80052..98416
/note="assembly_fragment"
98517..119303
/note="assembly_fragment"
119404..167677
/note="assembly_fragment"
BASE COUNT 46556 a 37571 c 36546 g 45599 t 1405 others
ORIGIN

```

```

Query Match 35.7%; Score 581; DB 69; Length 167677;
Best Local Similarity 77.9%; Pred. No. 3,7e-127;
Matches 775; Conservative 0; Mismatches 190; Indels 30; Gaps 5;

Qy 8 catggagtgtagccgagaggaagcatgtgcccgtcggtgcgcgtgctgtgctgccc 67
Db 25328 CACTGGGCATTACCAAGGAAGCAAGCATGCTGCCATCAGCTAGCTGCTGGCCACAC 25269
Qy 68 tctgtgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 127
Db 25268 TGGGGCAGTGTGG-----CCCAAGAGGCTGCGCTACGCTGGAGGAGTGTA 25222

```

```

Qy 128 gaggcgtgctgaccagctctgccaggagacagcgtgactctgacctgcccggggtagagc 187
Db 25221 GTGATGTGCTGA-----CCAGGATATGATTCCTCCCTGACCTGCTCAGAGGAGAAC 25170
Qy 188 cggaagacaatgcacatgttccactgttgctcaggaagcgcgcgcgcgcgcgcgcgcgc 247
Db 25169 CTGAAATCATGCACACTGTCCACTGTGTGCACAGAGACTCCAGCGCAGGCTCAGC 25110
Qy 248 gcagatggcgtggcatgggaagagagcgtgctgctgaggtgcggtgcagctccagcactc 307
Db 25109 GCAGATGGGCTGGTGTGGGAAGAGGCTGCTTCTGAGGTGGTGCAGCTCTCGGACTCT 25050
Qy 308 gaaactattcatctaccgggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 367
Db 25049 GAAACTATTCTTCTGCTGCCGGCTGGCTGCCAGCAGG--TCTGTGCTTGTGTGGTGA 24992
Qy 368 ttccccccgagggagcccccagctctcctgctccggaagcgcgcgcgcgcgcgcgcgcgc 427
Db 24991 TTTCTCCTGAGGAGCCTCAGCTCTCCTGCTTCTTGAAGAGCCCCCTCAGTGACATTGG 24932
Qy 428 gtgagtggtgctcctcgagacacccccatccctgacgacaaaggcgtgctctgtgtgagga 487
Db 24931 GTGAATAGAGTCTCTGGAGTCAAGGTTCTGAGTC----AAAGCTGTGCTATTGCTGAG 24876
Qy 488 agtttcagaaacagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 547
Db 24875 AGTTTCAGAACTGTCAGGCAGAACTCTTCCAGGAGCGGTGCTCAGTATTCTCAGAGT 24816
Qy 548 agaagttctcctgccagttagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 607
Db 24815 AGAAGTT---CTGCCAGTTGGCAGTGCAGAGGGAGATTACTCTTTCTATACAGTGTCC 24759
Qy 608 tgcgcgtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 667
Db 24758 TGTGTGTACCAACAGATTGTTGGAGCAAGTTTCAGCAAAACCCAAATATTAGAGGTTAT 24699
Qy 668 gaattctgcagcctgctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 727
Db 24698 GAATCCTGCAGTCCGACCCACCTGTCAACATCAGTTCATTGCTGTGGCCAGAAAGCCCT 24639
Qy 728 gctggtcagtgctcactggaagaccccccactcctggaactcatctttctacagactac 787
Db 24638 GCTGGCTCAACGTCACCTAGCAGACACCCCTCCTGGAACCTTATATTCTTACAGACTAT 24579
Qy 788 ggttgagctcagatcggtgacgcgtcaagacatcacaacatgcacacatgcagtgatgc 847
Db 24578 GGTTTGAGCTTTGATACCTGGCTAAATAGTCAAAAATGTTCAATAACATGATGCCAAG 24519
Qy 848 acctccagcatcactgtgtcatccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 907
Db 24518 ATCTCCAACATCAGTGTGTCAATTCACAACACCTGGAAGGCATGAGGCACACACAGC 24459
Qy 908 ttctgcccagagagagtcgggcaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 967
Db 24458 TTCAGGCCCCAGAGGAGCTGGGGCAAGGCTTGTGAAGTGAAGTGGAGCCCGAGGCTCAT 24399
Qy 968 gcagccttgacagaatccagggagtcctccagct 1002
Db 24398 GAACCCCTTGGGAGACTCCAGAGAGTCTCCAGCT 24364

```

```

RESULT 10
LOCUS AC015889/c
DEFINITION Homo sapiens chromosome 17 clone RP11-251E22 map 17, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
ACCESSION AC015889
VERSION AC015889.3 GI:7108383
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



```
misc_feature /note="assembly_fragment:00827"
101617..102936
misc_feature /note="assembly_fragment:00912"
103037..114706
misc_feature /note="assembly_fragment:01184"
114807..115872
misc_feature /note="assembly_fragment:01349"
115973..117049
misc_feature /note="assembly_fragment:01482"
117150..136261
misc_feature /note="assembly_fragment:01515"
136362..160914
misc_feature /note="assembly_fragment:01593"
161015..168014
misc_feature /note="assembly_fragment:00637
clone_end:77
vector_side:right"
BASE COUNT 48401 a 34909 c 34023 g 48440 t 2241 others
ORIGIN
```

```
Query Match 35.5%; Score 577.8; DB 40; Length 168014;
Best Local Similarity 77.7%; Pred. No. 2.1e-126;
Matches 773; Conservative 0; Mismatches 192; Indels 30; Gaps 5;

QY 8 catgagtgtagcgcgaggaagcatgctgcccgtcgctgcgcgtgctggtgctgcc 67
Db 1537 CACTGGCATTAGCCCAAGGAAGCAGTCGTGCCATCAGCTGAGTGTCTGGCCACAC 1478

QY 68 tgcgtgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 127
Db 1477 TCGCGGCAGTGTGG-----CCCAAGAGGCTGCCCTAGCTGGAGGCAGTGA 1431

QY 128 gaggcgtgctgaccagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 187
Db 1430 GTGATGTGCTGA-----CCAGGATACGTGCTCCCTGACCTGTCCAGAGGGAGAAC 1379

QY 188 cggagacaatccactgttactggtgctcaggaagcgcgcgcgcgcgcgcgcgcgcgc 247
Db 1378 CTGAAATCATGCCACTGTCCACTGGTTCACAGGACTCCACAGCGCAGCTCAGCCCA 1319

QY 248 gcagatggcgtgctggaagagcgtgctgctgagtcgctgagtcgctgagtcgctg 307
Db 1318 GCAGATGGCGTGTGGGAGGAGGCTGCTTCTGAGGTGGTGAGCTGCTGCGACTG 1259

QY 308 gaaactattcatgctaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 367
Db 1258 GAAACTATTCTTGTGCTGCCGGGTGGCTGCCAGCAGG--TCTGTGCTTTGTTGGTGGATG 1201

QY 368 ttcccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 427
Db 1200 TTTCTCTCTGAGGAGCCTCAGCTCTCTGCTTCTGAGAGAGCCCCCTCAGTGACATGTTT 1141

QY 428 gtgagtggtggtcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 487
Db 1140 GTGAATAGAGTCTCTGGAGTCAAGGTTCTGAGTC----AAAGCTGTGCTATTGCTGAGAA 1085

QY 488 agttcagaagcagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 547
Db 1084 AGTTTCAGAACTGTGAGGAGCAACTCTTCCAGGAGCCGTGTGCTGATTTCTCAGGAGTCCC 1025

QY 548 aqaagtctctccgcagttgacgtccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 607
Db 1024 AGAAGTT---CTGCCAGTTGGCAGTGGCCAGAGGAGATTAATCTTCTATACAGTGTCCC 968

QY 608 tdtgcgtgcgcagtagtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 667
Db 967 TGTGTGTCACCAACAGTATTGGGAGCAGTTCAGCAAAACCCAAATATTAGAGGGTTATG 908

QY 668 gaatttgagcctgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 727
Db 907 GAACTCTGCAGTCCGACCCACCTGTCAACATCACATGCATTCATTGCTGTGGCCAGAAAGCCCT 848
```

```
QY 728 gctggctcagtgctacactggaagacagccccacactcctggaactcatctttctcagactac 787
Db 847 GCTGGCTCAACGCTCACCTAGCAAGACCCCACTCTCTGGAACTTATATTTCTACAGACTAT 788
QY 788 ggttgagctcagatgcggcgtgaacggtcctcaaaacattccacaacatggatggtcaagg 847
Db 787 GGTGTTGAGCTTTGATACCTGGCTAAATAGTCAAAAAATGTTTCATAAGCATGGATGCCAAGG 728
QY 848 acctccagcatcactgtgtcatccacgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 907
Db 727 ATCTCCAAACATCAGTGTGTGATTCACAACACCTCGGAAGCATGAGGCACACACACACAC 668
QY 908 ttctgctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 967
Db 667 TTCAGSCCCAGGAGGAGCTGGGCAAGGCTTGTGAAGTAAGTGGAGGCCAGAGGTCATGG 608
QY 968 gcacgccttgacacgaatccacagcagcagcagcagcagcagcagcagcagcagcagcagc 1002
Db 607 GAATCCTTTGGCAGACTCCAGGAGTCTCTCCAGCT 573
```

```
RESULT 12
AL161629
LOCUS
DEFINITION
AL161629 168372 bp DNA HTG 31-MAR-2000
SEQUENCING IN PROGRESS ***, 15 unordered pieces.
ACCESSION
AL161629
VERSION
AL161629.1 GI:7263517
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Plumb, B.
Direct Submission
Submitted (31-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in
progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known: 800 n's separate
segments. Contig_ID: 00031 Length: 2661bp
Contig_ID: 00066 Length: 10973bp
Contig_ID: 00107 Length: 14391bp
Contig_ID: 00291 Length: 6776bp
Contig_ID: 00297 Length: 1517bp
Contig_ID: 00330 Length: 11940bp
Contig_ID: 00630 Length: 3326bp
Contig_ID: 00849 Length: 35707bp
Contig_ID: 00850 Length: 4251bp
Contig_ID: 00921 Length: 17363bp
Contig_ID: 00996 Length: 2470bp
Contig_ID: 01013 Length: 13935bp
Contig_ID: 01079 Length: 11376bp
Contig_ID: 01086 Length: 16007bp
Contig_ID: 01168 Length: 4479bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved. 2661: contig of 2661 bp in length
* 1
* 2662 3461: gap of 800 bp
* 3462 14434: contig of 10973 bp in length
* 14435 15234: gap of 800 bp
* 15235 29625: contig of 14391 bp in length
```

*	28626	30425:	gap of	800 bp
*	30426	37201:	contig of	6776 bp in length
*	37202	38001:	gap of	800 bp
*	38002	39518:	contig of	1517 bp in length
*	39519	40318:	gap of	800 bp
*	40319	52258:	contig of	11940 bp in length
*	52259	53058:	gap of	800 bp
*	53059	56384:	contig of	3326 bp in length
*	56385	57184:	gap of	800 bp
*	57185	92891:	contig of	35707 bp in length
*	92892	93691:	gap of	800 bp
*	93692	97942:	contig of	4251 bp in length
*	97943	98742:	gap of	800 bp
*	98743	116105:	contig of	17363 bp in length
*	116106	116905:	gap of	800 bp
*	116906	119375:	contig of	2470 bp in length
*	119376	120175:	gap of	800 bp
*	120176	134110:	contig of	13935 bp in length
*	134111	134910:	gap of	800 bp
*	134911	146286:	contig of	11376 bp in length
*	146287	147086:	gap of	800 bp
*	147087	163093:	contig of	16007 bp in length
*	163094	163893:	gap of	800 bp
*	163894	168372:	contig of	4479 bp in length.

FEATURES

```

1. .168372
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="q21.33-22.2"
/clone="RP11-406A20"
/clone_lib="pcc1-112"

```

BASE COUNT	ORIGIN	44685 a	34503 c	34478 g	43492 t	11214 others
	/clone_rid=					
	afca 11.2					

[illegible]

Db	68026	AGTTTCAAGAACTGTGACGGCAGAACTCTTCACAGAGCGGTGCAGTATTCTCAGGAGTCCC	68085	
Qy	548	agaagttctcctgcaggttagcagtcgccggaggagacagctctttctacatagtgcca	607	
Db	68086	AGAAAGTT--CTGCCAGTTGGCAGTGCACAGAGGAGATTACTCTTTCTATACAGTGTCCC	68142	
Qy	608	tgtcgtctgcagtagtgtcggagacaagttcagcaaaaactcaaacctttcagggttgtg	657	
Db	68143	TGTGTGTACCAACAGATTGGGAGCAAGTTCAGCAAAACCCAAATATTAGAGGGTTATG	68202	
Qy	668	gaatcttgacgctgtatcccgctgcgaactcaactcagtcacgtgcgctggccagaaaacccc	727	
Db	68203	GAATCCTGCAGTCGCGACCCACCTGTCTCAACATCATCAGTCAATTGTGTGGCCAGAAAGCCCT	68262	
Qy	728	qctggctcagtgctcacctggcaagacccccacactcctggaactcatctttctacagactac	787	
Db	68263	GCTGGCTCAACGTCACCTAGCAGAGACCCCCACTCCTTGAAGTATTATTTCTACAGACTAT	68322	
Qy	788	ggtttgagctcagatatacgggctgaacggtcaagaacattcaacaatgatgatgcgaag	847	
Db	68323	GGTTTGAGCTTTGTATACCTGGCTAAATAGTCAAAAATGTTCTAATCAATGGATGCCAAGG	68382	
Qy	848	acctccagcatcaactgtgtcatccacgacgcctggagcggccttgaggcagctgggtgcagc	907	
Db	68383	ATCTCCAAACATCAGTGTGTCTATTCAACAACCTGGAAGGCGATGAGCGACGACACAGC	68442	
Qy	908	ttcgtgccagagagagttcggcaagcgagtcagcagtgatgagagcccgaggccatgg	967	
Db	68443	TTCAGGCCCAAGGAGAGCTGGGGCAAGGCTTGTGAATGATGTGGAGGCCAGAGTCAATGG	68502	
Qy	968	gcaqgccttggacagaatccaggagctccacgt	1002	
Db	68503	GAATCCTTTGGCGACACTCCAGGAGTCTCCAGCT	68537	

RESULT 13

```

FEATURES             1098 bp      mRNA      PRI      21-MAR-1995
HsILB2R              Human mRNA for interleukin BSF-2 (B-cell differentiation factor).
DEFINITION
ACCESSION            X04602
VERSION              X04602.1  GI:33849
KEYWORDS              B-cell differentiation factor; interleukin BSF-2; signal peptide.
SOURCE
ORGANISM             Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1098)
Hirano, T., Yasukawa, K., Harada, H., Taga, T., Watanabe, Y.,
Matsuda, T., Kashiwamura, S.I., Nakajima, K., Koyama, K., Iwamatsu, A.,
Tsunasawa, S., Sakiyama, F., Matsui, H., Takahara, Y., Taniguchi, T. and
Kishimoto, T.
Complementary DNA for a novel human interleukin (BSF-2) that
induces B lymphocytes to produce immunoglobulin
Nature 324 (6092), 73-76 (1986)
87065033             Location/Qualifiers
1..1098
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="TCL-Nal"
34..117
/product="put. signal peptide (AA -28 to -1)"
34..672
/note="precursor polypeptide (AA -28 to 184)"
/codon_start=1
/db_protein_id="CAA28268.1"
/db_xref="GI:33850"
/db_xref="SWISS-PROT:P05231"
/translation="MNSFSTAFGCVAFVSLGLLVLPAAPFVPPGDSKDVAAPIHRI
QPLTSSERIDKQIRYILDIGISALRKETCNKSMCESSEKALAEENLLPKMAEKDGGCF
QSGNEETFCIVK1ITGLLEFVYLQNRFESEGEQARAVOMSTKVLIQFLKKAK
LDATITPPTTNASLLTQLQONQWLQDTHLLIRSEKFLQSLRALRQM"
sig_peptide
CDS

```

```
mat_peptide      118..669
                  /product="put. mature polypeptide (AA 1-184)"
misc_feature     250..258
                  /note="pot. N-glycosylation site"
misc_feature     547..555
                  /note="pot. N-glycosylation site"
misc_feature     1072..1077
                  /note="put. polyA signal"
polyA_site       1098
                  /note="polyA site"
BASE COUNT      333 a 237 c 226 g 302 t
ORIGIN
Query Match      34.7%; Score 565.2; DB 9; Length 1098;
Best Local Similarity 99.5%; Pred. No. 1.8e-123;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1057 ccagttacccccggagaagattccaaagatgtagccgccccacacagacagccactcacc 1116
DB 118 CCAGTACCCCGAGGAGAGATTCCAAAGATGTAGCGCCGCCACACAGACAGCCACTCACC 177
QY 1117 tcttcagaacgaattgacaaacaattcgtgtacatctcgtcagcggcatctcagccctgaga 1176
DB 178 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGCGGCATCTCAGCCCTGAGA 237
QY 1177 aaggagacatgtaacagagtaacatgtgtgaagcagcaagagagcactggcagaaaaac 1236
DB 238 AAGGAGACATGTAAACAGAGTAAATGTGTGAAGCAGCAAGAGGCATGGCAGAAAAAC 297
QY 1237 aaactgaaccttcacaaagatggtgtgaaaaagatggatgtttcccaatctggattcaatgag 1296
DB 298 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAATCTGGATTCAATGAG 357
QY 1297 gagacttgctggtgaaatacatcactggtcttttgagatttgaggatatacctagagtagc 1356
DB 358 GAGACTTGCTGCTGGTGAATATCATCACTGTGCTTTTGGAGTTTGGAGTATACCTAGAGTAC 417
QY 1357 ctccagaacagatttgagagtagtgaggaacaagccagagctgtgcagatgagtagacaaa 1416
DB 418 CTCAGAACAGATTGAGAGTAGTAGGAAACAAAGCCAGACAGCTGTGCAGATGATGACAAA 477
QY 1417 gtctgataccgtctcgcagaaaaaggcaaaagatctagatgcaataaccacccctgac 1476
DB 478 GTCTGTATCCAGTTCCTGCAGAAAAAGGCAAAAGATCTAGATGCAATAACCAACCCCTGAC 537
QY 1477 caaacacaaaatgcagcctgtgcagcaagcgtgcagggcacagaaccagtggtgtgcaggac 1536
DB 538 CCAACACAAAATGCCAGCCTGTGTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 597
QY 1537 atgacaactcatctcattctgcagcctttaaggagttcctcagtcagccagcctgaggct 1596
DB 598 ATGACAACTCATCTCATTTCTGGCAGCTTTAAGGAGTTTCTCGAGTCCAGCTTGAGGGCT 657
QY 1597 cttcggaatgtagcatgggcacgcctcga 1626
DB 658 CTTGCGCAAAATGTAGCATGGCACCCTCAGA 687

RESULT 14
E03737
LOCUS      E03737      1102 bp      RNA      PAT      29-SEP-1997
DEFINITION cdna encoding human B-cell differentiation factor.
ACCESSION  E03737
VERSION    E03737.1  GI:2171952
KEYWORDS   JP 1992169599-A/1.
SOURCE     Homo sapiens.
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
           Primates; Catarrhini; Hominoidea; Homo.
REFERENCE  1 (bases 1 to 1102)
AUTHORS   Yasueda,H., Nagase,K., Kawai,M., Fukuhara,K. and Matsui,Y.
TITLE     VARIANT HUMAN BCBF

JOURNAL      Patent: JP 1992169599-A 1 17-JUN-1992;
COMMENT      AJINOMOTO CO INC
              OS Homo sapiens (human)
              PN JP 1992169599-A/1
              PD 17-JUN-1992
              PF 30-OCT-1990 JP 1990290704
              PI YASUEDA HISASHI, NAGASE KAZUO, KAWAI MISAOKO, FUKUHARA KENICHI,
              PM MATSUI YUTAKA
              PC C07K13/00,C12N15/24,C12P21/02//A61K37/02,A61K37/02,A61K37/02,
              PC (C12P21/02,
              PC C12R1:19);
              CC strandedness: Double;
              CC topology: Linear;
              CC hypothetical: No;
              CC anti-sense: No;
              FH Key
              FH Location/Qualifiers
              FT 5'UTR <1..35
              FT CDS 36..674
              FT /product='B-cell differentiation factor' FT
              sig_peptide 36..119 /product='signal peptide of B-cell FT
              FT differentiation factor'
              FT mat_peptide 120..671
              FT /product='B-cell differentiation factor' FT
              3'UTR 675..1102.
FEATURES
Source
Location/Qualifiers
1..1102
/organism='Homo sapiens'
/db_xref='taxon:9606'
BASE COUNT 336 a 238 c 226 g 302 t
ORIGIN

Query Match      34.7%; Score 565.2; DB 5; Length 1102;
Best Local Similarity 99.5%; Pred. No. 1.8e-123;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1057 ccagttacccccggagaagattccaaagatgtagccgccccacacagacagccactcacc 1116
DB 120 CCAGTACCCCGAGGAGAGATTCCAAAGATGTAGCGCCGCCACACAGACAGCCACTCACC 179
QY 1117 tcttcagaacgaattgacaaacaattcgtgtacatctcgtcagcggcatctcagccctgaga 1176
DB 180 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCTGACGGCATCTCAGCCCTGAGA 239
QY 1177 aaggagacatgtaacagagtagtaacatgtgtgaagcagcaagagagcactggcagaaaaac 1236
DB 240 AAGGAGACATGTAAACAGAGTAACATCTGTGAAAGCAGCAAAAGAGGCATGGCAGAAAAAC 299
QY 1237 aaactgaaccttcacaaagatggtgtgaaagcagcaagagagcactggcagaaaaac 1296
DB 300 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAATCTGGATTCAATGAG 359
QY 1297 gagacttgctggtgaaaaatcatcactggtcttttgagtttgaggtatcacctagagtagc 1356
DB 360 GAGACTTGCTGCTGGTGAATATCATCACTGGTCTTTTGGAGTTTGGAGTATACCTAGAGTAC 419
QY 1357 ctccagaacagatttgagagtagtgagggaacaagccagagcactgtgcagatgcagtagacaaa 1416
DB 420 CTCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGATGAGTACAAA 479
QY 1417 gtctgataccgtctcgcagaaaaaggcaaaagatgagatgcttccaatctgagttcaatgag 1476
DB 480 GTCTGTATCCAGTTCCTGCAGAAAAAGGCAAAAGATCTAGATGCAATAACCAACCCCTGAC 539
QY 1477 ccaaacacaaaatgccagcctgtgcagaaagcactgcagggcacagaccagtggtgtgcaggac 1536
DB 540 CCAACACAAAATGCCAGCCTGTGTGACGAAGCTGCAGGCACAGAACCAAGTGGCTGCAGGAC 599
QY 1537 atgacaactcatctcattctgcagcctttaaggagtttctcagtcagccagcctgaggct 1596
DB 600 ATGACAACCTCATCTCATTTCTGCGCAGCTTTAAGGAGTTTCTTCGAGTCCAGCTTGAGGGCT 659
```

QY 1597 cttcggcaaatgtagcatggcaccctcga 1626
|||||
Db 660 CTTCCGCAAAATGTAGCATGGCCACCTCAGA 689
|||||

RESULT 15
HUMIL6C 1102 bp mRNA PRI 06-JAN-1995
LOCUS Human interleukin 6 (B-cell stimulatory factor-2) mRNA, complete
DEFINITION cds.
ACCESSION M29150
VERSION M29150.1 GI:186349
KEYWORDS B-cell stimulatory factor-2; BSF-2; cytokine; interleukin 6;
transmembrane glycoprotein.
SOURCE Human cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1102)
AUTHORS Tonouchi,N., Miwa,K., Karasuyama,H. and Matsui,H.
TITLE Deletion of 3' untranslated region of human BSF-2 mRNA causes
stabilization of the mRNA and high-level expression in mouse NIH3T3
cells
JOURNAL Biochem. Biophys. Res. Commun. 163 (2), 1056-1062 (1989)
MEDLINE 89391958
FEATURES
source Location/Qualifiers
1..1102
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="7p21-p14"
36..674
/gene="IL6"
36..674
/gene="IL6"
/note="interleukin 6"
/codon_start=1
/db_xref="GDB:G00-120-748"
/protein_id="AA59154.1"
/db_xref="GI:307063"
/translation="MNSFSTSAFGPVAFSLGILLVLPAAFPVPPCEDSKDVAAPHR
QPLTSSRIDKQIRYILDGIALRKETCNKSNMCSKEALAEENLNLPMKAEKDCGF
QSGFNEETCLVKITTELEFEVLEYLQNFSESEQARAVQMTSKVLIQFLQKKAKN
LDAITTPDTTNASLLTKLQANQWLODMTTHLILRSFKREFLOSSURLRQM"

BASE COUNT 336 a 238 c 226 g 302 t
ORIGIN

Db 420 CTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA 479
|||||
QY 1417 gtccctgattccagttccctgcagaaaaagcgaagaatctagatgcaataaccacccctgtac 1476
|||||
Db 480 GTCCCTGATCCAGTTCTCTGCAGAAAAAGGCAAGAATCTAGATGCATTAACCAACCCCTGAC 539
|||||
QY 1477 ccaaccacaaaatgccagcctctgcaggaagctgcagggcacagaaacagtggtgcaggac 1536
|||||
Db 540 CCAACCCACAAAATGCCAGCCTGTGACGAAGCTGCAGGACACAGAACAGTGGCTGCAGGAC 599
|||||
QY 1537 atgacaactcactcattctgcgagcgtttaaggagttcctcagctccagctcaaggct 1596
|||||
Db 600 ATGACAACCTCACTCTCATTTCTGCGCAGCTTTAAGGAGTTCTCTCAGTCCAGCCTGAGGGCT 659
|||||
QY 1597 cttcggcaaatgtagcatggcaccctcga 1626
|||||
Db 660 CTTCCGCAAAATGTAGCATGGCCACCTCAGA 689
|||||

Search completed: August 9, 2000, 07:00:26
Job time: 61940 sec

Query Match 34.7%; Score 565.2; DB 10; Length 1102;
Best Local Similarity 99.5%; Pred. NO. 1.8e-123;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1057 ccagttaccctccaggaagattccaaagattagcgcgccacacagacagaccactcacc 1116
|||||
Db 120 CCAGTACCCCCAGGAGAGATTCCAAAGATGTAGCCGCCCCACACAGACGCCACTCACC 179
|||||
QY 1117 tcttcagaacgaattgacaaacaaattcgtacatcctctgcagcggcatctcagccctcaga 1176
|||||
Db 180 TCTTCAGACGAATTGACAAACAAATTCGGTACATCCTCGACGGCATCTCAGCCCTGAGA 239
|||||
QY 1177 aaggagacatgtacaagagtaacatgtgtgaagcagcaaaagagcactggcagaaaaac 1236
|||||
Db 240 AAGGAGACATGTAAACAGAGTAACTGTGTGAAGCAGAAAGAGGCACTGGCAGAAAAAC 299
|||||
QY 1237 aacctgaacctccaagatgctgaaaaagattgagtgcttccaatcttgattcaatgag 1296
|||||
Db 300 AACCTGAACCTTCCAAGATGGCTGAAAAGATGGATGTTCCATCTGGATTCAATGAG 359
|||||
QY 1297 gagacttgcttggtgaaatcatcactggtcttttggagtttgaggtataccttagagtac 1356
|||||
Db 360 GAGACTTGCTGCTGTAATAATCATCACTGCTCTTTGGAGTTTGAGGTATACCTAGAGTAC 419
|||||
QY 1357 ctcagaacagatttgagagtagtgaggaaacagccagagctgtgcagatgagtacaaaa 1416
|||||

MPSEARCH

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 10 16:03:23 2000; MasPar time 40.32 Seconds
Tabular output not generated. 902.719 Million cell updates/sec

Title: >US-09-142-471-2
Description: (1-525) from US09142471.pep
Perfect Score: 3803
Sequence: 1 MGVGCALLAALLAAGAAL.....LILRSFKFLQSLRALRQM 525

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrnbl12

1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 50.204; Variance 95.919; scale 0.523

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1320	34.7	440	11	INTERLEUKIN 6 RECEPTOR	3.24e-249
2	1239	32.6	209	6	INTERLEUKIN-6 (FRAGMENT)	1.69e-231
3	814	21.4	209	6	INTERLEUKIN 6 (FRAGMENT)	1.71e-139
4	810	21.3	205	6	INTERLEUKIN 6 (FRAGMENT)	1.23e-138
5	804	21.1	208	6	INTERLEUKIN 6 PRECURSOR	2.35e-137
6	748	19.7	160	6	INTERLEUKIN-6 (FRAGMENT)	2.04e-125
7	725	19.1	207	6	INTERLEUKIN 6 (FRAGMENT)	1.57e-120
8	539	14.2	210	11	IL-6 (FRAGMENT)	1.71e-81
9	413	10.9	372	11	CILIARY NEUTROTROPHIC F	9.20e-56
10	401	10.5	432	11	INTERLEUKIN-11 RECEPTOR	2.34e-53
11	400	10.5	432	11	INTERLEUKIN-11 RECEPTO	3.71e-53
12	397	10.4	66	6	INTERLEUKIN 6 RECEPTOR	1.48e-52
13	381	10.0	94	6	INTERLEUKIN 6 (FRAGMENT)	2.28e-49
14	377	9.9	422	4	INTERLEUKIN-11 RECEPTO	1.42e-48
15	329	8.7	101	11	INTERLEUKIN 6 (FRAGMENT)	3.77e-39
16	252	6.6	204	14	ORF K2.	1.50e-24
17	252	6.6	204	14	INTERLEUKIN-6 HOMOLOG	1.50e-24
18	205	5.4	422	4	CYTOKINE-LIKE FACTOR-1	4.14e-16
19	182	4.8	228	11	CYTOKINE RECEPTOR-LIKE	3.59e-12
20	179	4.7	296	6	PROLACTIN RECEPTOR SHO	1.14e-11

21	180	4.7	581	6	O46561	PROLACTIN RECEPTOR LON	7.76e-12
22	168	4.4	229	4	O75269	HUMAN CYTOKINE RECEPTO	7.44e-10
23	163	4.3	229	4	O14213	CYTOKINE RECEPTOR PREC	4.80e-09
24	161	4.2	346	13	O93404	PROLACTIN RECEPTOR (FR	1.01e-08
25	154	4.0	316	11	O35545	INTRON 5-INSERTED FORM	1.30e-07
26	151	4.0	335	6	P79203	PROLACTIN RECEPTOR (FR	3.84e-07
27	142	3.7	206	4	O16354	PROLACTIN RECEPTOR (FR	9.28e-06
28	130	3.4	217	6	O46386	PROLACTIN RECEPTOR (FR	5.57e-04
29	130	3.4	329	6	O9XS05	INTERLEUKIN 12 P40 SUB	5.57e-04
30	130	3.4	625	6	O9XS92	PROLACTIN RECEPTOR PRE	5.57e-04
31	129	3.4	895	11	O62960	LEPTIN RECEPTOR.	7.77e-04
32	124	3.3	194	6	O02708	GRANULOCYTE COLONY-STI	4.01e-03
33	124	3.3	229	6	O27950	ERYTHROPOIETIN RECEPTO	4.01e-03
34	124	3.3	229	6	O28206	ERYTHROPOIETIN RECEPTO	4.01e-03
35	124	3.3	344	13	O42403	ATTACHMENT REGION BIND	4.01e-03
36	125	3.3	471	11	O9WTN9	MRNA, COMPLETE CDS, SI	2.89e-03
37	126	3.3	874	11	P97378	INTERLEUKIN 12 RECEPTO	2.09e-03
38	125	3.3	1084	10	O43010	SUCROSE PHOSPHATE SYNT	2.89e-03
39	121	3.2	313	5	O77284	BEADEX/DLMO PROTEIN.	1.05e-02
40	121	3.2	738	5	O02402	INSOLUBLE PROTEIN.	1.05e-02
41	122	3.2	862	4	O99665	IL-12 RECEPTOR BETA2.	7.64e-03
42	122	3.2	881	13	O57519	GPI30PL.	7.64e-03
43	123	3.2	1165	6	O02671	TRANSMEMBRANE LEPTIN R	5.54e-03
44	121	3.2	1571	4	O60469	DOWN SYNDROME CELL ADH	1.05e-02
45	121	3.2	1896	4	O60468	DOWN SYNDROME CELL ADH	1.05e-02

ALIGNMENTS

RESULT 1
ID Q00343 PRELIMINARY; PRT; 440 AA.
AC Q00343;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 RECEPTOR, ALPHA PRECURSOR
DE (MUTANT INTERLEUKIN-6 RECEPTOR).
GN IL6RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE: 90278354.
RA SUGITA T., TOTSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,
RA KISHIMOTO T.;
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomagenesis."
RL J. Exp. Med. 171:2001-2009(1990).
CC -1- MISCELLANEOUS: THIS PROTEIN IS A ABNORMAL INTERLEUKIN-6 RECEPTOR.
CC IN THE CDNA ENCODING THE ABNORMAL INTERLEUKIN-6 RECEPTOR THE
CC REGION CORRESPONDING TO ITS INTRACYTOPLASMIC DOMAIN WAS REPLACED
CC WITH A LONG TERMINAL REPEAT OF THE INTRACISTERNAL A PARTICLE (IAP)
CC GENE. A MEMBER OF THE ENDOGENOUS PRORETROVIRAL-LIKE ELEMENTS
CC PRESENT IN THE GENOME OF MUS MUSCULUS.
DR EMBL: X51976; CAA36238.1;
DR PIR: JLO144; JLO144.
DR HSSP: P14787; IAN3.
DR MGD: MGI:105304; IL6ra.
DR PFAM: PF00041; fn3; 1.
DR PFAM: PF00047; ig; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT CHAIN 1 19
FT DOMAIN 1 385
FT DOMAIN 20 357
FT DOMAIN 20 357
FT DOMAIN 43 96
FT TRANSMEM 358 385
FT DOMAIN 386 440
FT DOMAIN 386 440
FT DISULFID 47 92


```
RL Immunogenetics 43:190-195(1996).
DR EMBL; I46803; AAB01429.1; -.
DR HSP; P05231; 1ALU.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 205 AA; 23266 MW; C853C8DF CRC32;

Query Match 21.3%; Score 810; DB 6; Length 205;
Best Local Similarity 60.7%; Pred. No. 1.23e-138;
Matches 111; Conservative 36; Mismatches 35; Indels 1; Gaps 1;

Db 21 PGPGLGDFKDDTSDRLYLTSPTDKTEALIKYILGKISAMRKEMCEKYDKCNESKEALAEN 80
QY 342 PVPFGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 81 NLNPKMAEKDGCFCGSGFNQETCLMRITTCGLLEYQIYLDYQNEYEYEDKAEIAVQISSK 140
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVLEYLQNRFSSESEQARAVQMSTK 461
Db 141 ALAQILRQKVKNPDEVTTPDPTTNASLMNNLQSONDDMKNTKIILRLSLENFLQFSLR 200
QY 462 VLIOFLQKRAKNLDAITTPDPTTNASLLTKLQAOQN-WLODMTTHILRSFKREFLOSSLR 520
Db 201 AIR 203
QY 521 ALR 523

RESULT 5
ID Q9X780 PRELIMINARY; PRT; 208 AA.
AC Q9X780;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 PRECURSOR.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Monodontidae;
OC Delphinapterus.
RN [1]
RP SEQUENCE FROM N.A.
RA ST-LAURENT G., DE GUISE S., FOURNIER M., ARCHAMBAULT D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AAD42929.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SEQUENCE 208 AA; 23456 MW; 0FA70646 CRC32;

Query Match 21.1%; Score 804; DB 6; Length 208;
Best Local Similarity 60.1%; Pred. No. 2.35e-137;
Matches 110; Conservative 36; Mismatches 36; Indels 1; Gaps 1;

Db 24 PGPGLGDFKDDTSDRLYLTSPTDKTEALIKYILGKISAMRKEMCEKYDKCNESKEALAEN 83
QY 342 PVPFGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 84 NLNPKMAEKDGCFCGSGFNQETCLMRITTCGLLEYQIYLDYQNEYEYEDKGSIEAVQISSK 143
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVLEYLQNRFSSESEQARAVQMSTK 461
Db 144 ALAQILRQKVKNPDEVTTPDPTTNASLMNNLQSONDDMKNTKIILRLSLENFLQFSLR 203
QY 462 VLIOFLQKRAKNLDAITTPDPTTNASLLTKLQAOQN-WLODMTTHILRSFKREFLOSSLR 520
Db 204 AVR 206
QY 521 ALR 523

RESULT 6
ID O97535 PRELIMINARY; PRT; 160 AA.
AC O97535;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
RN [1]
RP SEQUENCE FROM N.A.
RA ECHEVERRY S.J., HERNANDEZ E., MORENO A., PATARROYO M.E., MURILLO L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
RT in 4 Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014505; AAD01531.1; -.
DR HSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 160 AA; 17855 MW; EF6090C3 CRC32;

Query Match 19.7%; Score 748; DB 6; Length 160;
Best Local Similarity 87.5%; Pred. No. 2.04e-125;
Matches 105; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 29 PVPGLGDSKEVAAPNRQLTSTEQIDKHRYILEGIALRKEICDKSNMCESSKEALAEN 88
QY 342 PVPFGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 89 NLNPKMAEKDGCFCGSGFNEETCLTKITGLLEFEVLEYLQNRFSSESEQAVQMSTK 148
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVLEYLQNRFSSESEQARAVQMSTK 461

RESULT 7
ID Q28403 PRELIMINARY; PRT; 207 AA.
AC Q28403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Enhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Mustelidae; Enhydra.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96163018.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,
RA STOTT J.L., FERRICK D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL; I46804; AAB01428.1; -.
DR HSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 207 AA; 23527 MW; 0F2CAC62 CRC32;

Query Match 19.1%; Score 725; DB 6; Length 207;
Best Local Similarity 54.3%; Pred. No. 1.57e-120;
Matches 100; Conservative 42; Mismatches 40; Indels 2; Gaps 2;

Db 26 PGPGLGDSKDDATSNRPPLTSADKMEFIKFIILGKISALRNEMCDKYNKCESKEVLAEN 85
QY 342 PVPFGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKSNMCESSKEALAEN 401
Db 86 NLNPKLAEKDRFCQSRFNOETCLTRITTCGLQEFQIHLKYLESNYEGNKDHAIVYSTK 145
QY 402 NLNPKMAEKDGCFCGSGFNEETCLVKITGLLEFEVLEYLQNRFSSESEQARAVQMSTK 461
```

RESULT	9	
ID	O88507	PRELIMINARY; PRT; 372 AA.
AC	O88507;	
DT	01-NOV-1998	(TRENBLrel. 08, Created)
DT	01-NOV-1998	(TRENBLrel. 08, Last sequence update)
DT	01-MAY-1999	(TRENBLrel. 10, Last annotation update)
DT	DE	CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
GN	CNTRF.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
EC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BRAIN, SKELETAL MUSCLE:	
MA	MAEDA M., YAGUCHI N., HANYU C., NAKATA Y., ONODA N., TULIN E.E.,	
KO	KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;	
RT	"Mouse homolog of human ciliary neurotrophic factor receptor.";	
RRL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF068615; AAC25711.1; -.	
DR	PFAM; PF00041; fn3; 1.	
DR	PFAM; PF00047; lg; 1.	
KW	Signal.	

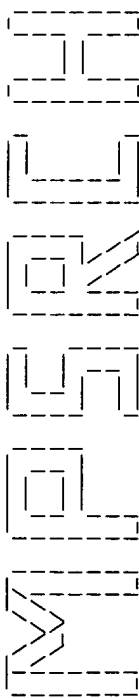
RESULT	10	
ID	Q64385	PRELIMINARY;
AC	Q64385;	PRT; 432 AA.
DT	01-JAN-1998	(TREMELrel. 05, Created)
DT	01-JAN-1998	(TREMELrel. 05, Last sequence update)
DT	01-NOV-1999	(TREMELrel. 12, Last annotation update)
DE	INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)	
DE	(IL1LRA1ALPHA) (IL1LRA1).	
DE	IL1LRA1 OR IL1LRA OR ETL2 OR ETL2/IL11 REC.	
GN	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6 X CBA; TISSUE=LIVER;	
RC	MEDLINE: 95045367.	
RX	HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,	
RA	COUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.;	
RT	"Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130	
RT	for high affinity binding and signal transduction.";	
RL	EMBO J. 13:4765-4775(1994).	
RL	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BALE/C, AND C57BL/6; TISSUE=EMBRYO;	
RC	NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,	
RA	GUENET J.L., GOSSLER A.;	
RL	Dev. Biol. 166:521-542(1994).	
RL	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BALE/C, AND C57BL/6;	
RC	GOSSLER A.;	
RL	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.	
RL	[4]	
RP	SEQUENCE FROM N.A.	
RC	MEDLINE: 97129000.	
RX	BILINSKI P., HALL M.A., NEUHAUS H., GISEL C., HEATH J.K., GOSSLER A.;	
RA	"Two differentially expressed interleukin-11 receptor genes in the	
RT	mouse genome.";	
RL	Biochem. J. 320:359-363(1996).	
RL	[5]	

[illegible][illegible]

DF 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
RN [1]
RP SEQUENCE FROM N.A.
RA HEINE H., DELUDE R.D., MONKS B., GOLENBOCK D.T.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044667; AAC02100.1; -
DR HSSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 11749 MW; D1DA362A CRC32;
Query Match 8.7%; Score 329; DB 11; Length 101;
Best Local Similarity 41.2%; Pred. No. 3.77e-39;
Matches 40; Conservative 28; Mismatches 28; Indels 1; Gaps 1;
Db 5 NDGCYQGYGYNWEICLLKITSGLLDYQIYLEFVTNNVQDNKKDKARVIQSTTKTILSQIFKQ 64
QY 411 KDGCFQSGFNEETCLVRIITGLLEFEVYLEVLIQNR-ESSEEQARAVQMSTKVLIQFLQK 469
Db 65 EVKDPDKIVMPSPSKAILIEKLESQKQWPRTKTIEL 101
QY 470 KAKNLDAITTPDPTTNASLTLKLAQANQWLQDMWTHL 506

Search completed: Thu Aug 10 16:05:57 2000
Job time : 154 secs.

inis Page Blank (uspio)



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.

Copyright (c) 1993-1998 University of Edinburgh, U.K.

Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 10 16:01:55 2000; MasPar time 17.41 Seconds

Tabular output not generated. 934.508 Million cell updates/sec

Title: >US-09-142-471-2

Description: (1-525) from US09142471.pep

Perfect Score: 3803

Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSKFELQSSLRALRQW 525

Scoring table: PAM 150

Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot38

1:swissprot

Statistics: Mean 50.832; Variance 91.281; scale 0.557

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description Pred. No.

1 2398 63.1 468 1 IL6A_HUMAN INTERLEUKIN-6 RECEPTOR 0.00e+00

2 1356 35.7 462 1 IL6A_RAT INTERLEUKIN-6 RECEPTOR 1.31e-273

3 1320 34.7 460 1 IL6A_MOUSE INTERLEUKIN-6 RECEPTOR 3.19e-265

4 1287 33.8 212 1 IL6_HUMAN INTERLEUKIN-6 RECEPTOR 1.53e-257

5 1257 33.1 212 1 IL6_MACFA INTERLEUKIN-6 RECEPTOR 1.45e-250

6 1251 32.9 212 1 IL6_MACMU INTERLEUKIN-6 RECEPTOR 3.59e-249

7 1244 32.7 212 1 IL6_CERTO INTERLEUKIN-6 RECEPTOR 1.52e-247

8 814 21.4 209 1 IL6_PROVI INTERLEUKIN-6 RECEPTOR 1.43e-148

9 810 21.3 205 1 IL6_ORCOR INTERLEUKIN-6 RECEPTOR 1.16e-147

10 806 21.2 208 1 IL6_HORSE INTERLEUKIN-6 RECEPTOR 9.40e-147

11 801 21.1 212 1 IL6_PIG INTERLEUKIN-6 RECEPTOR 1.28e-145

12 786 20.7 207 1 IL6_CANFA INTERLEUKIN-6 RECEPTOR 3.26e-142

13 786 20.7 208 1 IL6_FELCA INTERLEUKIN-6 RECEPTOR 3.26e-142

14 693 18.2 208 1 IL6_BOVIN INTERLEUKIN-6 RECEPTOR 3.27e-121

15 683 18.0 208 1 IL6_CAPHI INTERLEUKIN-6 RECEPTOR 5.77e-119

16 680 17.9 208 1 IL6_SHEEP INTERLEUKIN-6 RECEPTOR 2.72e-118

17 654 17.2 207 1 IL6_MARMO INTERLEUKIN-6 RECEPTOR 1.83e-112

18 560 14.7 211 1 IL6_MOUSE INTERLEUKIN-6 RECEPTOR 1.45e-91

19 558 14.7 211 1 IL6_RAT INTERLEUKIN-6 RECEPTOR 4.00e-91

20 491 12.9 125 1 IL6_MUSVI INTERLEUKIN-6 (IL-6) (1.97e-76

21 407 10.7 372 1 CNTR_RAT CILIARY NEUTROPHIC F 2.48e-58

22 403 10.6 372 1 CNTR_HUMAN CILIARY NEUTROPHIC F 1.76e-57

23 373 9.8 362 1 CNTR_CHICK CILIARY NEUTROPHIC F 3.88e-51

24	212	5.6	831	1	PRLR_CHICK	PROLACTIN RECEPTOR PRE	7.54e-19
25	205	5.4	831	1	PRLR_MELGA	PROLACTIN RECEPTOR PRE	1.50e-17
26	179	4.7	201	1	MGF_CHICK	MYELOMONOCYTIC GROWTH	7.51e-13
27	179	4.7	581	1	PRLR_BOVIN	PROLACTIN RECEPTOR PRE	7.51e-13
28	172	4.5	830	1	PRLR_COLLI	PROLACTIN RECEPTOR PRE	1.26e-11
29	165	4.3	630	1	PRLR_ORENI	PROLACTIN RECEPTOR PRE	2.04e-10
30	155	4.1	917	1	IL6B_MOUSE	INTERLEUKIN-6 RECEPTOR	9.94e-09
31	152	4.0	616	1	PRLR_RABIT	PROLACTIN RECEPTOR PRE	3.13e-08
32	144	3.8	622	1	PRLR_HUMAN	PROLACTIN RECEPTOR PRE	6.31e-07
33	140	3.7	610	1	PRLR_RAT	PROLACTIN RECEPTOR PRE	2.75e-06
34	141	3.7	918	1	IL6B_HUMAN	INTERLEUKIN-6 RECEPTOR	1.91e-06
35	139	3.7	918	1	IL6B_RAT	INTERLEUKIN-6 RECEPTOR	3.96e-06
36	137	3.6	581	1	PRLR_CEREL	PROLACTIN RECEPTOR PRE	8.18e-06
37	137	3.6	608	1	PRLR_MOUSE	PROLACTIN RECEPTOR PRE	8.18e-06
38	128	3.4	327	1	IL12B_MARMO	INTERLEUKIN-12 BETA CH	1.99e-04
39	130	3.4	329	1	IL12B_HORSE	INTERLEUKIN-12 BETA CH	9.91e-05
40	129	3.4	1162	1	LEPR_RAT	LEPTIN RECEPTOR PRECUR	1.41e-04
41	125	3.3	206	1	TWST_MOUSE	TWIST RELATED PROTEIN	5.63e-04
42	127	3.3	328	1	IL12B_HUMAN	INTERLEUKIN-12 BETA CH	2.82e-04
43	126	3.3	329	1	IL12B_FELCA	INTERLEUKIN-12 BETA CH	3.99e-04
44	126	3.3	329	1	IL12B_CANFA	INTERLEUKIN-12 BETA CH	3.99e-04
45	126	3.3	4393	1	PGSM_HUMAN	BASEMENT MEMBRANE-SPEC	3.99e-04

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	468 AA.
ID	IL6A_HUMAN			
AC	P08887;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (CD126			
DE	ANTIGEN).			
GN	IL6R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 88305347.			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RT	"Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2)			
RT	receptor".			
RL	Science 241:825-828(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RL	"Molecular structure of interleukin 6 receptor.";			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 91336983.			
RA	Schooltink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,			
RA	Kishimoto T., Heinrich P.C., Rose-John S.;			
RT	Structural and functional studies on the human hepatic interleukin-6			
RT	receptor. Molecular cloning and overexpression in HepG2 cells.";			
RL	Biochem. J. 277:659-664(1991).			
CC	-1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6			
CC	WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.			
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD126 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm".			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			


```
QY 180 VPEGSSFFIVSMCVSSVSGSKFTQTFQGGCIIQDPDPANITVAVARNRWLSVTWQ 239
    : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 237 DPESWDPYLLQFELRYRPVSKFTVWPLQVACHOCVHIDALRGVKKVHVVGRKEED 296
    || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 240 DPHSNSSFYRLFELRYRAERSKFTTWMVKDLQHCVHDAWSGLRHVVQLRQEERG 299
    || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 297 IGOWSKWSEVGTGTPWLAEPRTTPA 321
    || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 300 QGEWSEWSPAMGTPW-TESRPPA 323
    || : || : || : || : || : || : || : || : || : || : || : || : ||

RESULT 3
ID IL6A_MOUSE STANDARD; PRT; 460 AA.
AC P22272;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
GN IL6RA OR IL6R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RX MEDLINE; 90278354.
RA Sugita T., Totusaka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.;
RT "Functional murine Interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomagenesis."
RL J. Exp. Med. 171:2001-2009(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C3H; TISSUE=LIVER;
RA Florillo M.T., Ciliberto G., Dente L.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC -!- WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X51975; CAA36237.1; -
DR EMBL; X53802; CAA37810.1; -
DR PIR; JLO145; JLO145.
DR PIR; S14543; S14543.
DR HSSP; P16471; 1BP3.
DR MGD; MGI:105304; IL6RA.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; 1g; 1.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 460 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT DOMAIN 21 357 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 358 385 POTENTIAL.
FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 47 92 POTENTIAL.
```

```
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 150 150 POTENTIAL.
FT CONFLICT 374 374 A -> R (IN REF. 2).
SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 34.7%; Score 1320; DB 1; Length 460;
Best Local Similarity 55.1%; Pred. No. 3.19e-265;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLYVGTCTLLVALLAAPVALVLGSCRALEVANGTVTSPLCATVTLICPGKEAAGNVTIHW 60
  ||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1 MLAVGCCALLAALLAAPGAALAPRCPAQEVARGVLSLPGDSVTLTCGVEPEDNATVHW 60
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 61 VY----SGSQNRWTTGNTLVLRDVLSDGTGDLGSLNDHLVGTVPVPLVDVPPPEPKLS 116
  || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 61 VLRKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 117 CFRKNPLVNAICEWRPSSPTTKAVLFAKKTNTNGKSDFOVPCQYSQOLKSFSCQVE 176
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 121 CFRKSPLSNVCCWGPSTPTTKAVLVRKFQNSPAE-DFQEPCCQYSQESQKFSQCLA 179
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 177 ILEGDKVYHIVSLCVANSVSGSKSHNEAFHSLKMKVQDPDPANLVSAIPGRPRWLKVSQ 236
  : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 180 VPEGSSFFIVSMCVSSVSGSKFTQTFQGGCIIQDPDPANITVAVARNRWLSVTWQ 239
  : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 237 HPETWDPYLLQFELRYRPVSKFTVWPLQVACHOCVHIDALRGVKKVHVVGRKEED 296
  || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 240 DPHSNSSFYRLFELRYRAERSKFTTWMVKDLQHCVHDAWSGLRHVVQLRQEERG 299
  || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 297 LGOWSEWSEVGTGTPWLAEPRTTPA 321
  || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 300 QGEWSEWSPAMGTPW-TESRPPA 323
  || : || : || : || : || : || : || : || : || : || : || : || : ||

RESULT 4
ID IL6_HUMAN STANDARD; PRT; 212 AA.
AC P05231;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
DE (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).
GN IL6 OR IFNB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE; 87065033.
RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
RA Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
RT B lymphocytes to produce immunoglobulin."
RL Nature 324:73-76(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88082664.
RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
RA Nakai S., Kishimoto T.;
RT "Structure and expression of human B cell stimulatory factor-2
RT (BSF-2/IL-6) gene."
RL EMBO J. 6:2939-2945(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87067433.
RA May L.T., Helfgott D.C., Sehgal P.B.;
RT "Anti-beta-2-interferon antibodies inhibit the increased expression of
RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
RT structural studies of the beta 2 interferon involved.";
```

Thu Aug 10 17:13:52 2000

Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
[4]
RN SEQUENCE FROM N.A.
RP MEDLINE; 87053818.
RX Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
RA "Structure and expression of cDNA and genes for human
RT interferon-beta-2, a distinct species inducible by growth-stimulatory
cytokines.";
RL EMBO J. 5:2529-2537(1986).
[5]
RN SEQUENCE FROM N.A.
RP MEDLINE; 89391958.
RX Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
EScherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
[6]
RN SEQUENCE FROM N.A.
RP MEDLINE; 89391958.
RX Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
EScherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
[7]
RN SEQUENCE FROM N.A.
RP MEDLINE; 89391958.
RX Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
EScherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
[8]
RN SEQUENCE FROM N.A.
RP MEDLINE; 89391958.
RX Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
EScherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
[9]
RN SEQUENCE FROM N.A.
RP MEDLINE; 89391958.
RX Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
EScherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
[10]
RN SEQUENCE OF 30-63.
RP MEDLINE; 88154445.
RX van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
RA Billiau A.;
RT "Separation and comparison of two monokines with
lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
RL J. Immunol. 140:1534-1541(1988).
[11]
RN SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
RP MEDLINE; 95154344.
RX Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
RA Zillicotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
RT "Structure, stability and biological properties of a N-terminally
truncated form of recombinant human interleukin-6 containing a single
disulfide bond.";
RL Eur. J. Biochem. 227:573-581(1995).
[12]
RN DISULFIDE BONDS.
RP MEDLINE; 89286115.
RX Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RA "Disulfide structures of human interleukin-6 are similar to those of
human granulocyte colony stimulating factor.";
RL Arch. Biochem. Biophys. 272:144-151(1989).
[13]
RN MUTAGENESIS.
RP MEDLINE; 91243808.
RX Luetticken C., Kruegger A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an
alpha-helical structure of the C-terminus for biological activity of
human IL-6.";
RL FEBS Lett. 282:265-267(1991).
[14]
RN STRUCTURE BY NMR.
RP MEDLINE; 96134845.
RX Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
by NMR spectroscopy.";
RL Biochemistry 35:273-281(1996).
[15]
RN STRUCTURE BY NMR.
RP MEDLINE; 97303053.
RX Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6.";
RL J. Mol. Biol. 268:468-481(1997).
[16]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RP MEDLINE; 97224126.
RX Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: Implications for a novel
mode of receptor dimerization and signaling.";
RL EMBO J. 16:989-997(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; X04430; CAA28026.1; -
CC EMBL; M14584; AAA52728.1; -
CC EMBL; X04602; CAA28268.1; -
CC EMBL; Y00081; CAA68278.1; -
CC EMBL; M18403; AAA52729.1; -
CC EMBL; M29150; AAA59154.1; -
CC EMBL; X04402; CAA27990.1; -
CC EMBL; X04403; CAA27991.1; -
CC EMBL; M54894; AAC41704.1; -
CC EMBL; S56892; AAD13886.1; -
CC EMBL; A09363; CAA00839.1; -
CC PIR; A32648; IVHUB2.
CC PIR; A25921; A25921.
CC PDB; 1IL6; 04-FEB-98.
CC PDB; 2IL6; 04-FEB-98.
CC PDB; 1ALU; 03-JUN-98.
CC MIN; 147620; -
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN6.
CC PROSITE; PS00254; INTERLEUKIN6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT MUTAGEN 173 173
FT MUTAGEN 185 185
A->V: ALMOST NO LOSS OF ACTIVITY.
W->R: NO LOSS OF ACTIVITY.

FT MUTAGEN 204 204 S->P: 13% ACTIVITY.
FT MUTAGEN 210 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
SQ SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;

Query Match 33.8%; Score 1287; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.53e-257;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 PVPGGEDSKDVAAPHROPTSSERIDKQIRYILDGTSALRKETCNKSNMCESKEALAEN 88
QY 342 PVPGGEDSKDVAAPHROPTSSERIDKQIRYILDGTSALRKETCNKSNMCESKEALAEN 401
Db 89 NLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVQMSK 148
QY 402 NLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVQMSK 461
Db 149 VLIOFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 208
QY 462 VLIOFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 521
Db 209 LROM 212
QY 522 LROM 525

RESULT 5
ID IL6 MACFA STANDARD; PRT; 212 AA.
AC P79341.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB000554; BAA19148.1; -
CC HSSP; P05231; 21L6.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

Query Match 33.1%; Score 1257; DB 1; Length 212;
Best Local Similarity 95.7%; Pred. No. 3.59e-249;
Matches 176; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 29 PVPGGEDSKDVAAPHROPTSSERIDKQIRYILDGTSALRKETCNKSNMCESKEALAEN 88
QY 342 PVPGGEDSKDVAAPHROPTSSERIDKQIRYILDGTSALRKETCNKSNMCESKEALAEN 401
Db 89 NLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVQMSK 148
QY 402 NLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVQMSK 461
Db 149 VLIOFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 208
QY 462 VLIOFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSKFELQSSLA 521
Db 209 LROM 212
QY 522 LROM 525

RESULT 6
ID IL6 MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates";
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L26028; AAA99978.1; -
CC HSSP; P05231; 1AUU.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC CYTOKINE; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 POTENTIAL.
FT CARBOHYD 172 172 POTENTIAL.
SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCCAD CRC64;

Query Match 32.9%; Score 1251; DB 1; Length 212;
Best Local Similarity 95.7%; Pred. No. 3.59e-249;
Matches 176; Conservative 6; Mismatches 2; Indels 0; Gaps 0;


```
QY 402 NLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFFESSEQARAVQMSTK 461
DB 146 LLVQMLKKVKVSODEVTTDPDPTTDSLOAILKAQDKWLKHTTHILHLSLEDFLOFSLRA 205
QY 462 VLIQFLOKKAKNLDAITTPDPTTNASLLTKLOAQNWLOQDMTHLILRSFKFLOSSLRA 521
DB 206 VRIM 209
QY 522 LRQM 525

RESULT 9
ID IL6_ORCOR STANDARD; PRT; 205 AA.
AC Q28747;
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96163018.
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L46803; AAB01429.1; -
DR HSP; P05231; IALU.
DR PFAM; PF00489; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 21 BY SIMILARITY.
FT CHAIN 22 205 INTERLEUKIN-6.
FT DISULFD 64 70 BY SIMILARITY.
FT DISULFD 93 103 BY SIMILARITY.
FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;

Query Match 21.3%; Score 810; DB 1; Length 205;
Best Local Similarity 60.7%; Pred. No. 1.16e-147;
Matches 111; Conservative 36; Mismatches 35; Indels 1; Gaps 1;

DB 21 PGLPEDFKDDTTSRLYLTSPDKTEALIKYILGISAMRKEMCKYDKCNSKEALAE 80
QY 342 PVPFGEDSKVAAPHRQPLTSERIDKQIRYILDIGISALRKETCNKSNWCKEALAE 401
DB 81 NLNPKMAEKDCGFCGSGFNEETCLMRTTGLLEYQIYLDYLNQNEYGDKATEAVQISK 140
QY 402 NLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVLEYLQNRFFESSEQARAVQMSTK 461
```

```
DB 141 ALAQILRQVKNPDEVTTDPDPTTNASIMNLOSNDMMKNTKIILIRLSLENFLOFSLR 200
QY 462 VLIQFLOKKAKNLDAITTPDPTTNASLLTKLOAQNQWLQDMTHLILRSFKFLOSSLR 520
DB 201 AIR 203
QY 521 ALR 523

RESULT 10
ID IL6_HORSE STANDARD; PRT; 208 AA.
AC Q95181; O19007; O46568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Swiderski C.E., Horohov D.W.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RT "Cloning and expression of equine interleukin-6.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U64794; AAB87703.1; -
DR EMBL; AF005227; AAB62246.1; -
DR EMBL; AF041975; AAC04574.1; -
DR HSP; P05231; IALU.
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 208 INTERLEUKIN-6.
FT DISULFD 69 75 BY SIMILARITY.
FT DISULFD 98 108 BY SIMILARITY.
FT CARBOHYD 71 71 POTENTIAL.
FT CARBOHYD 184 184 POTENTIAL.
FT CONFLICT 4 5 LS -> FF (IN REF. 1).
FT CONFLICT 8 8 T -> A (IN REF. 3).
FT CONFLICT 137 137 I -> V (IN REF. 2).
FT CONFLICT 205 205 V -> I (IN REF. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 21.2%; Score 806; DB 1; Length 208;
Best Local Similarity 59.2%; Pred. No. 9.40e-147;
Matches 109; Conservative 42; Mismatches 29; Indels 4; Gaps 3;
```

```

Db 29 PLPLGED--E-TTSGPLLTADTKTKOHIKIVILGKISALKNMCNMFSCENSKVLAEN 85
|:| | | | | : : : : | | : : : : | | | | | : | : | | | | | | |
Qy 342 PVPGEKSDKVAAPHRQPLTSERIDKQIRYILDIGSALRKETCNKSNMCSSKEALAE 401
|:| | | | | : : : : | | : : : : | | | | | : | : | | | | | | |
Db 86 NLNPKMAKDCGQSGFNGTCLMKITTTGLSEFQIYLEYLQNEFKGKKNITKMTQISTK 145
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 402 NLNPKMAKDCGQSGFNGTCLMKITTTGLSEFQIYLEYLQNEFKGKKNITKMTQISTK 461
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 VLVOILQKMKNP-VITPDPPTAKSSLLAKLHSONEWLKNTHLILRSLEDFLOFSIRA 204
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 462 VLIOFLOKAKNLDATITPDPPTTNASLLTKLQAQNWQLQDMTHLILRSKFEFLQSSIRA 521
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 205 VRIM 208
| | |
Qy 522 LRQM 525
| | |

RESULT 11
ID IL6_PTG STANDARD; PRT; 212 AA.
AC P26893;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 91338547.
RA Richards C., Saklatvala J.;
RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
RT expression of mRNA in synovial fibroblasts in vitro.";
RL Cytokine 3:269-276(1991).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE; 92360284.
RA Mathialagan N., Bixby J.A., Roberts M.R.;
RT "Preimplantation conceptuses.";
RT Mol. Reprod. Dev. 32:324-330(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; M86722; AAC37333.1; -.
CC EMBL; M80258; AAC27127.1; -.
CC HSSP; P05231; IALU.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PROSITE; PS00254; INTERLEUKIN6.
CC PROSITE; PS00254; INTERLEUKIN.6; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 30 212 INTERLEUKIN-6.
CC FT DISULFID 72 78 BY SIMILARITY.
CC FT DISULFID 101 111 BY SIMILARITY.
CC FT CONFLICT 30 30 G -> E (IN REF. 2).
CC SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

```

```

Query Match 21.1%; Score 801; DB 1; Length 212;
Best Local Similarity 59.8%; Pred. No. 1.28e-145;
Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;

Db 34 EDKAGDATSKMLFTSPDKTEELIKYILGKISAMRKMCEKYEKSCNSKEVLAENNLNP 93
| | | | | : : : : | | | | | : | : | | | | | | |
Qy 347 EDSKDAAPHRQPLTSERIDKQIRYILDIGSALRKETCNKSNMCSSKEALAE 406
| | | | | : : : : | | | | | : | : | | | | | | |
Db 94 KMAEKDCGQSGFNGTCLMKITTTGLSEFQIYLEYLQNEFKGKKNITKMTQISTK 153
| | | | | | | | | | | | | | | | | | | | | | | | |
Qy 407 KMAEKDCGQSGFNGTCLMKITTTGLSEFQIYLEYLQNEFKGKKNITKMTQISTK 466
| | | | | | | | | | | | | | | | | | | | | | | | |
Db 154 LRQKGNPDKATTPNPTNAGLLQSQNEWMKNTKIILIRSLDFLOFSIRATIM 212
| : | | | | | | | | | | | | | | | | | | | | | | |
Qy 467 LQKAKNLDATITPDPPTTNASLLTKLQAQNWQLQDMTHLILRSKFEFLQSSIRAL 525
| | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
ID IL6_CANFA STANDARD; PRT; 207 AA.
AC P41323;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
[1]
RN SEQUENCE FROM N.A.
RX STRAIN-MONGREL;
RX MEDLINE; 94303924.
RA Kukielka G.L., Youker K.A., Hawkins H.K., Perrard J.L.;
RA Michael L.H., Ballantyne C.M., Smith C.W., Entman M.L.;
RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
RT reperfusion.";
RL Ann. N.Y. Acad. Sci. 723:258-270(1994).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; U12234; AAA83030.1; -.
CC HSSP; P05231; 2IL6.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PROSITE; PS00254; INTERLEUKIN6.
CC PROSITE; PS00254; INTERLEUKIN.6; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 POTENTIAL.
CC CHAIN 30 207 INTERLEUKIN-6.
CC FT DISULFID 67 73 BY SIMILARITY.
CC FT DISULFID 96 106 BY SIMILARITY.
CC SEQUENCE 207 AA; 22945 MW; 45540154EA9C0F50 CRC64;

Query Match 20.7%; Score 786; DB 1; Length 207;
Best Local Similarity 58.2%; Pred. No. 3.26e-142;
Matches 107; Conservative 37; Mismatches 40; Indels 0; Gaps 0;

Db 24 PGPIAGDSKDATNSPLTSANKVEELIKYILGKISALRKEMCKFNKDCSKEALAE 83
| | | | | | | | | | | | | | | | | | | | | | | | |
Qy 342 PVPGEKSDKVAAPHRQPLTSERIDKQIRYILDIGSALRKETCNKSNMCSSKEALAE 401
| | | | | | | | | | | | | | | | | | | | | | | | |

```

```

Db 84 NLHLPKLEKDCGQFSGFNOETCLTRITTLGLVBFQLHLNLLQNNYEGDKENKSVHMSTK 143
QY 402 NLNPKMAEKDCGQFSGFNEETCLVKIITGLLEFEVLYLQNRPFESSEQARAVQMSTK 461
Db 144 ILVQMLKSKVKNODEVTPPTDPTDASLQALQSQODECVKHTTHLILRSLEDFLQSLRA 203
QY 462 VLQFOFKKAKNLDAITPPTDPTNASLLTKLQONQWLODMTHLILRSFKEFLQSLRA 521
Db 204 VRIM 207
QY 522 LRQM 525

RESULT 13
ID IL6_FELCA STANDARD; PRT; 208 AA.
AC P41683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94162386.
RA Hasegawa A.; Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
RT "Molecular cloning of feline interleukin-6 cDNA.";
RL J. Vet. Med. Sci. 55:941-944(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-LYMPHOCYTES;
RX MEDLINE; 94052249.
RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
RT "Molecular cloning and characterization of a cDNA encoding feline
interleukin-6.";
RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L16914; AA16620.1; -
CC DR EMBL; D13227; BAA02507.1; -
CC DR HSSP; P05231; 2IL6.
CC DR PFAM; PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFMGF.
CC DR PRINTS; PR00434; INTERLEUKIN_6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 208 INTERLEUKIN-6.
FT FT 68 74 BY SIMILARITY.
FT DISULFID 97 107 BY SIMILARITY.
FT FT 2 2 T -> N (IN REF. 2).
FT CONFLICT 45 45 S -> P (IN REF. 2).
FT FT 133 133 E -> K (IN REF. 2).
FT CONFLICT 173 187 AKLSQDEWLRLHTTI -> LSCSHRRVAEHNH (IN
FT REF. 2).
FT CONFLICT 200 201 FS -> LR (IN REF. 2).
FT SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

```

```

Query Match 20.7%; Score 786; DB 1; Length 208;
Best Local Similarity 57.8%; Pred. No. 3.26e-142;
Matches 100; Conservative 40; Mismatches 33; Indels 0; Gaps 0;

Db 36 ATSNRLPLTSADKMEELIKVILGKISALKKEMCDNYKNKCEDSKALAEENLNLPKLAEKD 95
QY 353 AAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNWCESSKALAEENLNLPKLAEKD 412
Db 96 GCFOSGNETCLTRITTTGLOEFQIYLFKFLQDYEGDEENAKSVYTTNVLQMLKRGK 155
QY 413 GCFOSGNETCLVKIITGLLEFEVLYLQNRPFESSEQARAVQMSTKVLQFOFKKAK 472
Db 156 NODEVTPVPTVEVGLQAKLQSQDEWLRLHTTHLILRSLEDFLQSLRAVRIM 208
QY 473 NLDAITPPTDPTNASLLTKLQONQWLODMTHLILRSFKEFLQSLRAVRIM 525

RESULT 14
ID IL6_BOVIN STANDARD; PRT; 208 AA.
AC P26892;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-HOLSTEIN;
RX MEDLINE; 93076003.
RA Droogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
RT "Nucleotide sequence of bovine interleukin-6 cDNA.";
RL DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X57317; CAA40572.1; -
CC DR EMBL; S22162; S22162.
CC DR HSSP; P05231; 2IL6.
CC DR PFAM; PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFMGF.
CC DR PRINTS; PR00434; INTERLEUKIN_6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT FT 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT FT 38 38 POTENTIAL.
FT SEQUENCE 208 AA; 23758 MW; AOF000B9BA2EC341 CRC64;

Query Match 18.2%; Score 693; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 3.27e-121;
Matches 93; Conservative 46; Mismatches 39; Indels 4; Gaps 2;

Db 29 PGFLGDFDKNDTTPGRLTLTPPEKTEALIKRMVDKISAMRKEICEKNDECESSKETLAEN 88

```

Qy 342 PVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKRETCNKNMCESSKEALAE 401
Db 89 KLNLPKMEKDCGCFQSGFNQAIICLIRTAGLEQIYLDYLONEVEGNOENVRDLRKNIR 148
Qy 402 NLNLPKMAEKDCGCFQSGFNETCLVKIITGLLEFEVYLEYLONFESSEEQARAVQMSTK 461
Db 149 TLIQILKQKIADL--ITTP--ATNTDLEKMOSSNEWKNAKIILIRNLNLEFLQFSIRA 204
Qy 462 VLIQFLQKKAKNLDATITPDPPTTNASLLTKLQAOQNWLDQMTHTHLIRSFKEFLQSSIRA 521
Db 205 IR 206
Qy 522 LR 523

RESULT 15
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC Q28319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Capra.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97392354.
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
cells";
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D86569; BAA13118.1; -.
DR HSSP; P05231; 2IL6.
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 POTENTIAL.
SQ SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 18.0%; Score 683; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 5.77e-119;
Matches 93; Conservative 43; Mismatches 42; Indels 4; Gaps 2;

Db 29 PGPGEDEFKNDTTPSRLLTTPKTEALIKHIVDKISAIRKEICEKNDCEKSKETLAEN 88
Qy 342 PVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKRETCNKNMCESSKEALAE 401
Db 89 KLNLPKMEKDCGCFQSGFNQAIICLIRTAGLEQIYLDYLONEVEGNOENVRDLRKNIR 148
Qy 402 NLNLPKMAEKDCGCFQSGFNETCLVKIITGLLEFEVYLEYLONFESSEEQARAVQMSTK 461
Db 149 TLIQILKQKIADL--ITTP--ATNTDLEKMOSSNEWKNAKIILIRNLNLEFLQFSIRA 204
Qy 462 VLIQFLQKKAKNLDATITPDPPTTNASLLTKLQAOQNWLDQMTHTHLIRSFKEFLQSSIRA 521
Db 205 IR 206
Qy 522 LR 523

Qy 402 NLNLPKMAEKDCGCFQSGFNETCLVKIITGLLEFEVYLEYLONFESSEEQARAVQMSTK 461
Db 149 TLIQILKQKIADL--ITTP--ATNTDLEKMOSSNEWKNAKIILIRNLNLEFLQFSIRA 204
Qy 462 VLIQFLQKKAKNLDATITPDPPTTNASLLTKLQAOQNWLDQMTHTHLIRSFKEFLQSSIRA 521
Db 205 IR 206
Qy 522 LR 523

Search completed: Thu Aug 10 16:03:06 2000
Job time : 71 secs.

W A R E A
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:00:16 2000; MasPar time 27.06 Seconds
Tabular output not generated. 915.129 Million cell updates/sec

Title: >US-09-142-471-2
Description: (1-525) from US09142471.pep
Perfect Score: 3803
Sequence: 1 MLAVGCALLAALLAAGPAAAL.....LILRSFKFELQSSLRALRQM 525

Scoring table: PAM 150
Gap 11
Searched: 142080 seqs, 47172406 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r64
1:p1r1 2:p1r2 3:p1r3 4:p1r4
Statistics: Mean 50.071; Variance 102.843; scale 0.487

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	ID	Description
1	2398	63.1	468	1 A41242	interleukin-6 recepto
2	1320	34.7	440	2 JI0144	interleukin-6 recepto
3	1320	34.7	460	2 JI0145	interleukin-6 recepto
4	1287	33.8	212	1 IVH082	interleukin-6 precurs
5	1090	28.7	462	1 A37986	interleukin-6 recepto
6	806	21.2	208	2 T09216	interleukin-6 precurs
7	801	21.1	212	2 I46590	interleukin 6 - pig
8	801	21.1	212	2 I46621	interleukin 6 - pi
9	693	18.2	208	1 A56610	interleukin-6 precurs
10	680	17.9	207	2 I46084	interleukin 6 - cat
11	679	17.9	208	1 S29549	interleukin-6 - sheep
12	560	14.7	211	1 ICMS6	interleukin-6 precurs
13	558	14.7	211	2 A34247	interleukin-6 precurs
14	407	10.7	372	2 T58141	ciliary neurotrophic
15	403	10.6	372	1 UHHUCN	ciliary neurotrophic
16	401	10.5	432	2 I48343	interleukin-11 recept
17	377	9.9	422	2 T37891	growth promoting acti
18	373	9.8	362	2 S60614	growth promoting acti
19	219	5.6	831	2 J01655	prolactin receptor pr
20	179	4.7	201	2 A42247	myelomonocytic growth
21	179	4.7	581	2 I45971	prolactin receptor -
22	172	4.5	830	2 I50455	prolactin receptor -
23	165	4.3	630	2 I51086	prolactin receptor -

24	155	4.1	917	2 I49699	glycoprotein 130 - mo
25	152	4.0	616	2 A30304	prolactin receptor 2
26	144	3.8	622	2 A40144	prolactin receptor lo
27	142	3.7	206	2 A57018	prolactin receptor -
28	140	3.7	310	2 A29884	prolactin receptor pr
29	140	3.7	412	2 A41070	prolactin receptor Nb
30	140	3.7	610	2 A36116	prolactin receptor 2
31	140	3.7	610	2 A34631	lactogen receptor 1 -
32	141	3.7	918	2 A36337	membrane glycoprotein
33	139	3.7	918	2 A44257	interleukin-6 signal
34	138	3.6	265	2 S14081	erythropoietin recept
35	137	3.6	292	2 I77525	prolactin receptor pr
36	137	3.6	303	2 I77524	prolactin receptor pr
37	137	3.6	608	2 I53269	prolactin receptor, 1
38	129	3.4	805	2 JC4897	leptin receptor, Ob-R
39	129	3.4	894	2 JC4797	leptin receptor, precu
40	129	3.4	895	2 S74225	leptin receptor, isof
41	129	3.4	1162	2 PC4184	leptin receptor, Ob-R
42	125	3.3	206	2 I53066	gene M-twist protein
43	127	3.3	328	2 A38957	interleukin 12B precu
44	124	3.3	894	2 S68437	leptin receptor (vari
45	125	3.3	1084	2 T04103	sucrose-phosphate syn

ALIGNMENTS

RESULT	1
ENTRY	A41242
TITLE	interleukin-6 receptor precursor - human
CONTAINS	interleukin-6 receptor, soluble form
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 22-Jun-1999
ACCESSIONS	A41242; J00080; S17468; A61459; S14621
REFERENCE	A41242 Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T. Science (1988) 241:825-828 Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor. #cross-references NUID:88305347
#accession	A41242
#molecule_type	mRNA
#residues	1-468
#label	YAM
#cross-references	GB:M20566; NID:gl86346; PID:g307062
REFERENCE	JU0080 Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T. Proc. Jpn. Acad. (1988) 64:209-211 Molecular structure of interleukin 6 receptor.
#accession	JU0080
#molecule_type	mRNA
#residues	1-468
#label	YA2
REFERENCE	S17468 Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, P.C.; Rose-John, S. Biochem. J. (1991) 277:659-664 Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells. #cross-references NUID:91336983
#accession	S17468
#molecule_type	mRNA
#residues	1-468
#label	SCH
#cross-references	EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581
#experimental_source	hepatoma cell line HepG2
REFERENCE	A61459 Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. (1989) 170:1409-1414 Soluble cytokine receptors are present in normal human urine. #cross-references NUID:90010793
#accession	A61459
#molecule_type	protein

```

##residues      20-49 ##label NOV
COMMENT          Through this receptor, interleukin-6 induces proliferation,
                  activation, and differentiation of various cell types.
COMMENT          This growth factor receptor does not have a tyrosine kinase domain.
GENETICS
#gene            GDB:IL6R
##cross-references GDB:127966; OMIM:147880
#map_position    lq21-lq21
CLASSIFICATION   #superfamily ciliary neurotrophic factor receptor; cytokine
                  receptor homology; immunoglobulin homology
KEYWORDS         acute phase; cytokine receptor; glycoprotein; transmembrane
                  protein
FEATURE
1-19             #domain signal sequence #status predicted #label SIG\
20-468          #product interleukin-6 receptor #status predicted #label
                  MAT\
20-363          #domain extracellular #status predicted #label EXT\
40-98            #domain immunoglobulin homology #label IMM2\
121-309          #domain cytokine receptor homology #label CRS\
364-386          #domain transmembrane #status predicted #label TMM\
387-468          #domain intracellular #status predicted #label INT\
47-96           #disulfide_bonds #status predicted\
55,93,221,245,350 #binding_site carbohydrate (Asn) (covalent) #status
                  predicted
SUMMARY          #length 468 #molecular-weight 51547 #checksum 4661

Query Match      63.1%; Score 2398; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCCALLAALAAPRCAPAEVARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60
QY 1 MLAVGCCALLAALAAPRCAPAEVARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60

Db 61 VLKRPAGSHPSWAGMGRLLRSVOLHDSGNYSCYRAGRAGTGVHLLVDVPPPEPQLS 120
QY 61 VLKRPAGSHPSWAGMGRLLRSVOLHDSGNYSCYRAGRAGTGVHLLVDVPPPEPQLS 120

Db 121 CFRKPSLNNVCEWGPSTPSLTAKVLLVRKFQNSPAE-DFQEPQCOYSQSFSCQLAV 180
QY 121 CFRKPSLNNVCEWGPSTPSLTAKVLLVRKFQNSPAE-DFQEPQCOYSQSFSCQLAV 180

Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFCGCGILQDPPANITVTAVARNPRLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFCGCGILQDPPANITVTAVARNPRLSVTWQD 240

Db 241 PHSWNSFFYLRFLRYRAERSKFTFTWMVKDLOHCHVHDANSGLRHVVQLRAQEEFG 300
QY 241 PHSWNSFFYLRFLRYRAERSKFTFTWMVKDLOHCHVHDANSGLRHVVQLRAQEEFG 300

Db 301 GEWSEWSPAMGTPWTESRPPA 323
QY 301 GEWSEWSPAMGTPWTESRPPA 323

RESULT 2
ENTRY      JLO144 #type complete
TITLE      interleukin-6 receptor precursor (clone lambda p1) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
ACCESSIONS JLO144
REFERENCE   JLO144
#authors    Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
#journal    J. Exp. Med. (1990) 171:2001-2009
#title      Functional murine interleukin 6 receptor with the
            intracisternal a particle gene product at its cytoplasmic
            domain: its possible role in plasmacytomagenesis.
#cross-references MUID:90278354
#accession  JLO144
#status      nucleic acid sequence not shown
##molecule_type mRNA
##residues   1-468 #label SIG
##cross-references GDB:127966; OMIM:147880; NID:952692; PID:952693
REFERENCE    JLO144
#authors    Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
#journal    J. Exp. Med. (1990) 171:2001-2009
#title      Functional murine interleukin 6 receptor with the
            intracisternal a particle gene product at its cytoplasmic
            domain: its possible role in plasmacytomagenesis.
#cross-references MUID:90278354
#accession  JLO144
#status      nucleic acid sequence not shown
##molecule_type mRNA

```

```

##residues      1-440 ##label SUG
##cross-references GDB:X51976; NID:953548; PID:CAA36238.1; PID:953549
CLASSIFICATION   #superfamily ciliary neurotrophic factor receptor; cytokine
                  receptor homology; immunoglobulin homology
KEYWORDS         cytokine receptor; transmembrane protein
FEATURE
1-19             #domain signal sequence #status predicted #label SIG\
20-440          #product interleukin-6 receptor #status predicted #label
                  MAT\
117-306          #domain cytokine receptor homology #label CRS\
358-385          #domain transmembrane #status predicted #label TRA
SUMMARY          #length 440 #molecular-weight 47901 #checksum 5876

Query Match      34.7%; Score 1320; DB 2; Length 440;
Best Local Similarity 55.1%; Pred. No. 5.97e-232;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLFTVGCTLLVALLAAPVALVGLSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHW 60
QY 1 MLAVGCCALLAALAAPRCAPAEVARGVLTSLPGDSVTLTCTCPGVEPEDNATVHW 60

Db 61 VY----SGSONRRTTGTNTLVLRDVLQSDTGDYLCSLNDHLVGTVPVLLVDVPPPEPKLS 116
QY 61 VLKRPAGSHPSWAGMGRLLRSVOLHDSGNYSCYRAGRAGTGVHLLVDVPPPEPQLS 120

Db 117 CFRKNPLVNAICEWRPSSTPSTTKAVLFAKINTNGKSDFOVPCQYSQLKSFSCQVE 176
QY 121 CFRKPSLNNVCEWGPSTPSLTAKVLLVRKFQNSPAE-DFQEPQCOYSQSFSCQLA 179

Db 177 ILEGDKYHYIVLCVANSVSGSKSHNEAFHSLKMWOPDPPANILVWSAIPGRPRWLKYSWQ 236
QY 180 VPEGDSSFYIVSMCVASSVSGSKFTQTFCGCGILQDPPANITVTAVARNPRLSVTWQ 239

Db 237 HPETWDPSTYVLYQLRYRPVWSKEFTVLLPVAQYOCVLDHALRGVKKVVOYGRKEELD 296
QY 240 PHSWNSFFYLRFLRYRAERSKFTFTWMVKDLOHCHVHDANSGLRHVVQLRAQEEFG 299

Db 297 LGQSEWSPAMGTPWTESRPPA 321
QY 300 GEWSEWSPAMGTPWTESRPPA 323

RESULT 3
ENTRY      JLO145 #type complete
TITLE      interleukin-6 receptor precursor (clone lambda 301) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
ACCESSIONS JLO145; S14543
REFERENCE   JLO144
#authors    Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
#journal    J. Exp. Med. (1990) 171:2001-2009
#title      Functional murine interleukin 6 receptor with the
            intracisternal a particle gene product at its cytoplasmic
            domain: its possible role in plasmacytomagenesis.
#cross-references MUID:90278354
#accession  JLO145
#status      nucleic acid sequence not shown
##molecule_type mRNA
##residues   1-460 #label SUG
##cross-references GDB:X51975; NID:949725; PID:CAA36237.1; PID:949726
REFERENCE    S14543
#authors    Fiorillo, M.T.; Ciliberto, G.; Dente, L.
#journal    submitted to the EMBL Data Library, July 1990
#title      Cloning and expression of murine IL-6 receptor.
#accession  S14543
#status      preliminary
##molecule_type mRNA
##residues   1-373, 'R', 375-460 #label FTO
##cross-references EMBL:X53802; NID:952692; PID:CAA37810.1; PID:952693
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine

```



```

##residues      1-212 #label BRA
##cross-references GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
REFERENCE
#authors      Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De
               Ley, M.; Billiau, A.
#journal      J. Immunol. (1988) 140:1534-1541
#title        Separation and comparison of two monokines with
               lymphocyte-activating factor activity: IL-1-beta and
               hydridoma growth factor (HGF). Identification of
               leukocyte-derived HGF as IL-6.
#cross-references MUID:88154445
#accession     A27601
##molecule_type protein
##residues     28-51,'X',53-57,'X',59,'X',61 #label VAM1
#accession     B27601
##molecule_type protein
##residues     30-56,'XX',59-61,'X',63 #label VA2
#accession     A60400
#authors      Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
#journal      J. Immunol. (1990) 144:1808-1816
#title        The human lung fibroblast cell line, MRC-5, produces multiple
               factors involved with megakaryocytopoiesis.
#cross-references MUID:90171574
#accession     A60400
##molecule_type protein
##residues     30-43 #label YAM
REFERENCE
#authors      Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.;
               Takatsuki, F.; Shimizu, M.; Murashima, A.; Tsunasawa, S.;
               Sakiyama, F.; Kishimoto, T.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1987) 84:228-231
#title        Human beta-cell differentiation factor defined by an
               anti-peptide antibody and its possible role in autoantibody
               production.
#cross-references MUID:87092370
#accession     A29085
##molecule_type protein
##residues     29-42 #label HIR2
REFERENCE
#authors      Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.;
               Hara, T.; Ishikawa, H.; Arimura, H.; Konno, K.
#journal      Anticancer Res. (1991) 11:961-968
#title        Purification and characterization of human fibroblast derived
               differentiation inducing factor for human monoblastic
               leukemia cells identical to interleukin-6.
#cross-references MUID:91290785
#accession     A61159
##molecule_type protein
##residues     30-42 #label NOD
##experimental_source fibroblast
REFERENCE
#authors      Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno,
               A.
#journal      J. Mol. Cell. Immunol. (1989) 4:203-212
#title        Interleukin 6 is the principal cytolytic T lymphocyte
               differentiation factor for thymocytes in human leukocyte
               conditioned medium.
#cross-references MUID:90121567
#accession     A61462
##molecule_type protein
##residues     28-48 #label MIN
##experimental_source leukocyte-conditioned medium
REFERENCE
#authors      May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal,
               P.B.
#journal      Cytokine (1991) 3:204-211
#title        Marked cell-type-specific differences in glycosylation of
               human interleukin-6.
#cross-references MUID:91355644
#accession     A48419
##molecule_type protein
##residues     30-37,'X',39-40 #label MAY2
##experimental_source FS-4 fibroblasts

```

```

##note          sequence extracted from NCBI backbone
##note          this 28-30K form contained both N-linked and O-linked
               carbohydrate; a 25K form containing only N-linked
               carbohydrate was also found
#accession      C48419
##molecule_type protein
##residues      28-40 #label MAY3
##experimental_source FS-4 fibroblasts
##note          sequence extracted from NCBI backbone (NCBIP:63787)
               this 23-25K form contained O-linked but not N-linked
               carbohydrate
REFERENCE
#authors      JX0305
               Orita, T.; Oheda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.;
               Ochi, N.
#journal      J. Biochem. (1994) 115:345-350
#title        Polypeptide and carbohydrate structure of recombinant human
               interleukin-6 produced in chinese hamster ovary cells.
#cross-references MUID:94266765
#contents      annotation; modified sites in recombinant protein from CHO
               cells
REFERENCE
#accession      S04981
...
Note: remainder of annotations omitted.
Query Match      33.8%; Score 1287; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.14e-225;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 PVPFGESKDVAAHPHQPLTSSERIDKQIRYILDGTSALRKETCNKNMCESSKEALAE 88
|||||
QY 342 PVPFGESKDVAAHPHQPLTSSERIDKQIRYILDGTSALRKETCNKNMCESSKEALAE 401
|||||
Db 89 NLNLPKMAERKDCGQSGFNEETCLVKITGLLEFVYVLEYLQNRFSSEQAQAVQMSK 148
|||||
QY 402 NLNLPKMAERKDCGQSGFNEETCLVKITGLLEFVYVLEYLQNRFSSEQAQAVQMSK 461
|||||
Db 149 VLIQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLDQMTTHILRSKFQSSLR 208
|||||
QY 462 VLIQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLDQMTTHILRSKFQSSLR 521
|||||
Db 209 LRQM 212
|||||
QY 522 LRQM 525

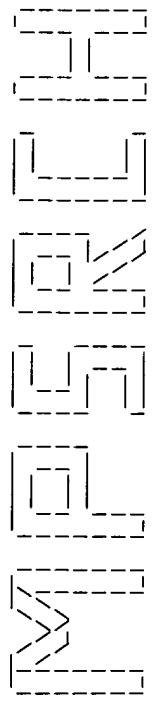
RESULT 5
ENTRY      A37986 #type complete
TITLE      interleukin-6 receptor precursor - rat
ALTERNATE_NAMES IL-6 receptor
ORGANISM    #formal_name Rattus norvegicus #common_name Norway rat
DATE        30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
              22-Jun-1999
ACCESSIONS  A37986
REFERENCE    A37986
#authors     Baumann, M.; Baumann, H.; Fey, G.H.
#journal     J. Biol. Chem. (1990) 265:19853-19862
#title       Molecular cloning, characterization and functional expression
               of the rat liver interleukin 6 receptor.
#cross-references MUID:91060602
#accession   A37986
##molecule_type mRNA
##residues   1-462 #label BAU
##cross-references GB:M58587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
               PID:g204922
COMMENT      After binding IL-6, this chain associates with a 130K glycoprotein
               that is essential for transmembrane signaling.
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
               receptor homology; immunoglobulin homology
KEYWORDS      acute phase; cytokine receptor; transmembrane protein
FEATURES
1-19
20-462
#domain signal sequence #status predicted #label SIG\
#product interleukin-6 receptor #status predicted #label
MAT\

```

[illegible]

Search completed: Thu Aug 10 16:01:39 2000
Job time : 83 secs.

1111 Page Blank (uspio)



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 10 16:06:14 2000; MasPar time 10.61 Seconds
Tabular output not generated. 714.244 Million cell updates/sec

Title: >US-09-142-471-2
Description: (1-525) from US09142471.pep
Perfect Score: 3803
Sequence: 1 MLAVGCCALLAALLAAPGAAL.....LILRSFKFQLQSSLRALRQM 525

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 35.092; Variance 199.930; scale 0.176

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.1	344	5	5480796-7	5.13e-167
2	2398	63.1	344	5	5171840-7	5.13e-167
3	2398	63.1	468	5	5480796-2	5.13e-167
4	2398	63.1	468	5	5171840-2	5.13e-167
5	2394	63.0	323	5	5480796-6	1.03e-166
6	2394	63.0	323	5	5171840-6	1.03e-166
7	1542	40.5	386	5	5480796-5	9.46e-103
8	1542	40.5	386	5	5171840-5	9.46e-103
9	1339	35.2	317	4	PCT-US95-0	Sequence 145, Applicat
10	1339	35.2	317	3	US-08-469-	Sequence 145, Applicat
11	1306	34.3	201	5	5171840-11	3.94e-85
12	1289	33.9	186	4	PCT-US94-1	Sequence 20, Applicati
13	1289	33.9	186	3	US-08-469-	Sequence 163, Applicat
14	1289	33.9	186	1	US-08-165-	Sequence 20, Applicati
15	1289	33.9	186	1	US-07-921-	Sequence 20, Applicati
16	1289	33.9	186	4	PCT-US95-0	Sequence 163, Applicat
17	1289	33.9	186	1	US-07-632-	Sequence 2, Applicatio
18	1289	33.9	186	1	US-07-745-	Sequence 20, Applicati
19	1287	33.8	184	2	US-08-567-	Sequence 2, Applicatio
20	1287	33.8	184	1	US-08-567-	Sequence 2, Applicatio
21	1287	33.8	184	5	5186931-1	Sequence 2, Applicatio
22	1287	33.8	185	1	US-07-918-	Sequence 2, Applicatio
23	1287	33.8	185	1	US-08-246-	Sequence 5, Applicatio

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	344 AA.
ID	5480796-7			
XX	xxxxxx			
AC				
DT				
DE	Patent No. 5480796			
XX				
CC	Patent No. 5480796			
CC	APPLICANT: KISHIMOTO, TADAMITSU			
CC	TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN			
CC	FOR HUMAN B CELL STIMULATORY FACTOR-2			
CC	NUMBER OF SEQUENCES: 8			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/07/907,650			
CC	FILING DATE: 02-JUL-1992			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: 298,694			
CC	FILING DATE: 19-JAN-1989			
CC	SEQ ID NO:7:			
CC	LENGTH: 344			
CC	SEQUENCE 344 AA; 38047 MW; 637889 CN;			
Query Match 63.1%; Score 2398; DB 5; Length 344;				
Best Local Similarity 100.0%; Pred. No. 5.13e-167;				
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	1	MLAVGCCALLAALLAAPGAALAPRRCPAQEARGVLTSLPGDSVTLTCPGVEPNATVHW	60	
Qy	1	MLAVGCCALLAALLAAPGAALAPRRCPAQEARGVLTSLPGDSVTLTCPGVEPNATVHW	60	
Db	61	VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDVPPPEQLS	120	
Qy	61	VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDVPPPEQLS	120	
Db	121	CFRKSPLSNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCOYSQESKQFSCOLAV	180	
Qy	121	CFRKSPLSNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCOYSQESKQFSCOLAV	180	
Db	181	PEGSSFFIVSMCVASSVSGSKFSKQTQTGGCGLQDPDPANITVAVARNPWLVSVTWQD	240	
Qy	181	PEGSSFFIVSMCVASSVSGSKFSKQTQTGGCGLQDPDPANITVAVARNPWLVSVTWQD	240	
Db	241	PHSNWSSFYRLRFELRYRAERSKTTTWMVKDLQHCYHDAWSGLRHVVQLRAQEEFGQ	300	
Qy	241	PHSNWSSFYRLRFELRYRAERSKTTTWMVKDLQHCYHDAWSGLRHVVQLRAQEEFGQ	300	

DE	Patent No.	5171840
xx		
CC	Patent No.	5171840
CC	APPLICANT:	KISHIMOTO, TADAMITSU
CC	TITLE OF INVENTION:	RECEPTOR PROTEIN FOR HUMAN B CELL
CC	STIMULATORY FACTOR-2	
CC	NUMBER OF SEQUENCES:	11
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/298,694
CC	FILING DATE:	19-JAN-1989
CC	SEQ ID NO:6:	
CC	LENGTH:	323
CC	SEQUENCE	323 AA; 35744 MW; 577074 CN;
CC	Query Match	63.0%; Score 2394; DB 5; Length 323;
CC	Best Local Similarity	100.0%; Pred. No. 1.03e-166;
CC	Matches	322; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db	1	MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Qy	1	MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db	61	VLRKPAAGSHPSRWAGHGRLLRLSRVOLHDSGNYSYRAGRPAAGTVHLLVDVPPEEQLS 120
Qy	61	VLRKPAAGSHPSRWAGHGRLLRLSRVOLHDSGNYSYRAGRPAAGTVHLLVDVPPEEQLS 120
Db	121	CFRKSPLSNVCEWGPRTSLTTKAVLLVRKFONSFAEDFOEPCOXSQESQKFCOLAV 180
Qy	121	CFRKSPLSNVCEWGPRTSLTTKAVLLVRKFONSFAEDFOEPCOXSQESQKFCOLAV 180
Db	181	PEGDSSFYIIVSMCVASSVGSKFSKTQTQFGCGIIQLPDPPTANITVTAVARNPRWLVSVTWD 240
Qy	181	PEGDSSFYIIVSMCVASSVGSKFSKTQTQFGCGIIQLPDPPTANITVTAVARNPRWLVSVTWD 240
Db	241	PHSNWSFYLRFELRYRAERSKFTTMMVKDLQHHCVIHDANGSLRHVVQLRAQEFGQ 300
Qy	241	PHSNWSFYLRFELRYRAERSKFTTMMVKDLQHHCVIHDANGSLRHVVQLRAQEFGQ 300
Db	301	GEWSEWSPKAMGTPTWTSRSPP 322
Qy	301	GEWSEWSPKAMGTPTWTSRSPP 322
RESULT	7	
ID	5480796-5	STANDARD; PRT; 386 AA.
AC	xxxxxx	
XX		
DT		
XX		
DE	Patent No.	5480796
CC		
CC	Patent No.	5480796
CC	APPLICANT:	KISHIMOTO, TADAMITSU
CC	TITLE OF INVENTION:	ANTIBODIES AGAINST THE RECEPTOR PROTEIN
CC	FOR HUMAN B CELL STIMULATORY FACTOR-2	
CC	NUMBER OF SEQUENCES:	8
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/907,650
CC	FILING DATE:	02-JUL-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	298,694
CC	FILING DATE:	19-JAN-1989
CC	SEQ ID NO:5:	
CC	LENGTH:	386
SQ	SEQUENCE	386 AA; 42734 MW; 827023 CN;
CC	Query Match	40.5%; Score 1542; DB 5; Length 386;
CC	Best Local Similarity	98.1%; Pred. No. 9.46e-103;
CC	Matches	212; Conservative 0; Mismatches 0; Indels 4; Gaps 2
Db	28	VDVPPPEEQLSCKFRKSPLSNVWC--GPRSTPEWSLTTKAVLLVRKFONSFAEDFOEPCQY 85
Qy	28	VDVPPPEEQLSCKFRKSPLSNVWC--GPRSTPEWSLTTKAVLLVRKFONSFAEDFOEPCQY 85

QY 110 VDVPEEPQLSCFRKSPLSNVVCEWGPSTP--SLTTKAVLLVRKFNQSPAEDEFQPCQY 167
Db 86 SOESQKFCQLAVPEGDSFFIVSMCVASSVSGSKFSKTQTFQGGCIIQPPDPANITVTAV 145
QY 168 SOESQKFCQLAVPEGDSFFIVSMCVASSVSGSKFSKTQTFQGGCIIQPPDPANITVTAV 227
Db 146 ARNPRWLSVTWQDPHNSWNSFFYRLRFELRYRAERSKFTFTWVKDLQHHCVIHDWNSGLR 205
QY 228 ARNPRWLSVTWQDPHNSWNSFFYRLRFELRYRAERSKFTFTWVKDLQHHCVIHDWNSGLR 287
Db 206 HVVQLRAQEEFGQGEWSEWSPAMGTPTWESRPPA 241
QY 288 HVVQLRAQEEFGQGEWSEWSPAMGTPTWESRPPA 323

RESULT 8
ID 5171840-5 STANDARD; PRT; 386 AA.
XX
AC xxxxxx
DT
DE
XX
XX
DE Patent No. 5171840
CC Patent No. 5171840
CC APPLICANT: KISHIMOTO, TADAMITSU
CC TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
CC STIMULATORY FACTOR-2
CC NUMBER OF SEQUENCES: 11
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/298,694
CC FILING DATE: 19-JAN-1989
CC SEQ ID NO:5:
CC LENGTH: 386
CC SEQUENCE 386 AA; 42734 MW; 827023 CN;

Query Match 40.5%; Score 1542; DB 5; Length 386;
Best Local Similarity 98.1%; Pred. No. 9.46e-103;
Matches 212; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

Db 28 VDVPEEPQLSCFRKSPLSNVV--GPRSTPEWSLTTKAVLLVRKFNQSPAEDEFQPCQY 85
QY 110 VDVPEEPQLSCFRKSPLSNVVCEWGPSTP--SLTTKAVLLVRKFNQSPAEDEFQPCQY 167
Db 86 SOESQKFCQLAVPEGDSFFIVSMCVASSVSGSKFSKTQTFQGGCIIQPPDPANITVTAV 145
QY 168 SOESQKFCQLAVPEGDSFFIVSMCVASSVSGSKFSKTQTFQGGCIIQPPDPANITVTAV 227
Db 146 ARNPRWLSVTWQDPHNSWNSFFYRLRFELRYRAERSKFTFTWVKDLQHHCVIHDWNSGLR 205
QY 228 ARNPRWLSVTWQDPHNSWNSFFYRLRFELRYRAERSKFTFTWVKDLQHHCVIHDWNSGLR 287
Db 206 HVVQLRAQEEFGQGEWSEWSPAMGTPTWESRPPA 241
QY 288 HVVQLRAQEEFGQGEWSEWSPAMGTPTWESRPPA 323

RESULT 9
ID PCT-US95-01185-145 STANDARD; PRT; 317 AA.
XX
AC xxxxxx
XX
DT
DE
XX
XX
DE Sequence 145, Application PC/TUS9501185
XX
CC Sequence 145, Application PC/TUS9501185
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
CC TITLE OF INVENTION: Protein
CC NUMBER OF SEQUENCES: 196
CC COMPUTER READABLE FORM:

QY 100 VDVPEEPQLSCFRKSPLSNVVCEWGPSTP--SLTTKAVLLVRKFNQSPAEDEFQPCQY 167
Db 86 SOESQKFCQLAVPEGDSFFIVSMCVASSVSGSKFSKTQTFQGGCIIQPPDPANITVTAV 145
QY 168 SOESQKFCQLAVPEGDSFFIVSMCVASSVSGSKFSKTQTFQGGCIIQPPDPANITVTAV 227
Db 146 ARNPRWLSVTWQDPHNSWNSFFYRLRFELRYRAERSKFTFTWVKDLQHHCVIHDWNSGLR 205
QY 228 ARNPRWLSVTWQDPHNSWNSFFYRLRFELRYRAERSKFTFTWVKDLQHHCVIHDWNSGLR 287
Db 206 HVVQLRAQEEFGQGEWSEWSPAMGTPTWESRPPA 241
QY 288 HVVQLRAQEEFGQGEWSEWSPAMGTPTWESRPPA 323

RESULT 10
ID US-08-469-318-145 STANDARD; PRT; 317 AA.
XX
AC xxxxxx
XX
DT
DE
XX
XX
DE Sequence 145, Application US/08469318
XX
CC Sequence 145, Application US/08469318
CC Patent No. 6022535
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
CC TITLE OF INVENTION: Protein
CC NUMBER OF SEQUENCES: 196
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/469,318
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/446,872
CC FILING DATE:
CC INFORMATION FOR SEQ ID NO: 145:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 317 amino acids
CC TYPE: amino acid

```

DT XX Sequence 20, Application PC/TUS9414179
DE XX
XX XX
CC XX Sequence 20, Application PC/TUS9414179
CC XX GENERAL INFORMATION:
CC CC APPLICANT: McCoy, John
CC CC APPLICANT: DiBlasio-Smith, Elizabeth
CC CC APPLICANT: Grant, Kathleen
CC CC APPLICANT: Lavallie, Edward R.
CC CC TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
CC CC TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
CC CC TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
CC CC NUMBER OF SEQUENCES: 29
CC CC CORRESPONDENCE ADDRESSES:
CC CC ADDRESSEE: Genetics Institute, Inc.
CC CC STREET: 87 CambridgePark Drive
CC CC CITY: Cambridge
CC CC STATE: Massachusetts
CC CC COUNTRY: U.S.A.
CC CC ZIP: 02140
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: Floppy disk
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: PCT/US94/14179
CC CC FILING DATE:
CC CC CLASSIFICATION:
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Meinert, M. C.
CC CC REGISTRATION NUMBER: 33,544
CC CC REFERENCE/DOCKET NUMBER: GI 5188D
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: (617) 876-1170
CC CC TELEFAX: (617) 876-5851
CC CC INFORMATION FOR SEQ ID NO: 20:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 186 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 33.9%; Score 1289; DB 4; Length 186;
Best Local Similarity 98.9%; Pred.No. 7.27e-84;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGSDSKDVAAHPHQPLTSSERIDKQIRYILDGISALRKETCKNKNMCESSKEALA 60
QY 340 VEPVPPGSDSKDVAAHPHQPLTSSERIDKQIRYILDGISALRKETCKNKNMCESSKEALA 399
      : |||||
Db 61 ENNLNLPKMAEKDGCFCQSGFNDETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVOMS 120
QY 400 ENNLNLPKMAEKDGCFCQSGFNDETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVOMS 459
      : |||||
Db 121 TKVLIOFLQKKAKNLDAITTPDPPTNASLLTKLQAONWLODMTHHLILRSKFELQSSL 180
QY 460 TKVLIOFLQKKAKNLDAITTPDPPTNASLLTKLQAONWLODMTHHLILRSKFELQSSL 519
      : |||||
Db 181 RALRQM 186
QY 520 RALRQM 525
      : |||||

RESULT 13
XX ID US-08-469-318-163 STANDARD; PRT; 186 AA.
XX AC xxxxxx
XX DT
XX XX
```

DE Sequence 163, Application US/08469318
XX
CC Sequence 163, Application US/08469318
CC Patent No. 6022535
CC GENERAL INFORMATION:
CC APPLICANT: Multivariant IL-3 Hematopoiesis Fusion
CC TITLE OF INVENTION: Protein
CC NUMBER OF SEQUENCES: 196
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/469,318
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA: 08/446,872
CC APPLICATION NUMBER:
CC FILING DATE:
CC INFORMATION FOR SEQ ID NO: 163:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;
SQ
Query Match 33.9%; Score 1289; DB 3; Length 186;
Best Local Similarity 98.9%; Pred. No. 7.27e-84;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 MAPVPGEDSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKNMCESSKEALA 60
QY 340 VEPVPGEDSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKNMCESSKEALA 399
Db 61 ENNLNLPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYLNRRFESSEEQARAVOMS 120
QY 400 ENNLNLPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYLNRRFESSEEQARAVOMS 459
Db 121 TKVLIQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSFKFEFLQSSL 180
QY 460 TKVLIQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSFKFEFLQSSL 519
Db 181 RALRQM 186
QY 520 RALRQM 525
RESULT 14
ID US-08-165-301A-20 STANDARD; PRT; 186 AA.
XX
AC xxxxxx
XX
DT
DE
XX
DE Sequence 20, Application US/08165301A
XX
CC Sequence 20, Application US/08165301A
CC Patent No. 5646016
CC GENERAL INFORMATION:
CC APPLICANT: McCoy, John
CC APPLICANT: DiBasio-Smith, Elizabeth
CC APPLICANT: Grant, Kathleen
CC APPLICANT: LaVallie, Edward R.
CC TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
CC TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
CC TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genetics Institute, Inc.

CC STREET: 87 CambridgePark Drive
CC CITY: Cambridge
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02140
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,301A
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meinhart, M. C. 33,544
CC REGISTRATION NUMBER: GI 51880
CC REFERENCE/DOCKET NUMBER:
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 876-1170
CC TELEFAX: (617) 876-5851
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;
SQ
Query Match 33.9%; Score 1289; DB 1; Length 186;
Best Local Similarity 98.9%; Pred. No. 7.27e-84;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 MAPVPGEDSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKNMCESSKEALA 60
QY 340 VEPVPGEDSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKNMCESSKEALA 399
Db 61 ENNLNLPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYLNRRFESSEEQARAVOMS 120
QY 400 ENNLNLPKMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLEYLNRRFESSEEQARAVOMS 459
Db 121 TKVLIQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSFKFEFLQSSL 180
QY 460 TKVLIQFLQKAKNLDATITPDPTTNASLLTKLQAOQWLODMTHLILRSFKFEFLQSSL 519
Db 181 RALRQM 186
QY 520 RALRQM 525
RESULT 15
ID US-07-921-848-20 STANDARD; PRT; 186 AA.
XX
AC xxxxxx
XX
DT
DE
XX
DE Sequence 20, Application US/07921848
XX
CC Sequence 20, Application US/07921848
CC Patent No. 5292646
CC GENERAL INFORMATION:
CC APPLICANT: McCoy, John
CC APPLICANT: LaVallie, Edward
CC TITLE OF INVENTION: Peptide and Protein Fusions To
CC TITLE OF INVENTION: Thioresoxin and Thioresoxin-Like Molecules
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genetics Institute, Inc.
CC STREET: 87 CambridgePark Drive
CC CITY: Cambridge
CC STATE: Massachusetts
CC COUNTRY: U.S.A.

CC ZIP: 02140
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/921,848
CC FILING DATE: 19920728
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/652,531
CC FILING DATE: 06-FEB-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/745,382
CC FILING DATE: 14-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Cserr, Luann
CC REGISTRATION NUMBER: 31,822
CC REFERENCE/DOCKET NUMBER: G15188A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 876-1170
CC TELEFAX: (617) 876-5851
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 33.9%; Score 1289; DB 1; Length 186;
Best Local Similarity 98.9%; Pred. No. 7.27e-84;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 1 MAPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCSKEALA 60
Qy 340 VEPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCSKEALA 399
Db 61 ENNLNPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVOMS 120
Qy 400 ENNLNPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVYLEYLQNRFFESSEEQARAVOMS 459
Db 121 TKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFELQSSL 180
Qy 460 TKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQONQWLQDMTTHLILRSFKFELQSSL 519
Db 181 RALROM 186
Qy 520 RALROM 525

Search completed: Thu Aug 10 16:07:05 2000
Job time : 51 secs.

This Page Blank (uspto)

W A R E L A

(TM)

Release 3.1A John F. Collins, BioComputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 15:59:00 2000; MasPar time 16.89 Seconds
Tabular output not generated. 736.366 Million cell updates/sec

Title: >US-09-142-471-2
Description: (1-525) from US09142471.pep
Perfect Score: 3803
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSFKFLOSSLRALRQM 525

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseqp

Statistics: Mean 37.337; Variance 202.644; scale 0.184

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				§					
Result No.	Score	Match	Length	DB	ID	Description	Pred. No.		
1	3803	100.0	525	1	W36846	Human fusion polypepti	8.73e-286		
2	3510	92.3	543	1	Y03164	Chimeric sIL-6R/IL-6 p	1.52e-262		
3	3335	87.7	500	1	W36847	Human fusion polypepti	1.13e-248		
4	2398	63.1	344	1	P90528	B cell stimulating fac	1.55e-174		
5	2398	63.1	468	1	P37215	IL-6 receptor.	1.55e-174		
6	2398	63.1	468	1	P90284	Sequence of a receptor	1.55e-174		
7	2391	62.9	360	1	W08004	Amino acid sequence of	5.54e-174		
8	2392	62.9	468	1	W98364	Interleukin-6 receptor	4.62e-174		
9	2391	62.9	592	1	W70797	Human interleukin-6R-a	5.54e-174		
10	2390	62.8	468	1	P90525	B cell stimulating fac	6.65e-174		
11	2373	62.4	468	1	W17371	Human interleukin-6 re	1.46e-172		
12	2351	61.8	323	1	P90527	B cell stimulating fac	7.97e-171		
13	2317	60.9	315	1	W70805	Amino acid sequence of	3.85e-168		
14	2110	55.5	1042	1	R70122	IL8-R type I-GPB 130 f	8.14e-152		
15	1534	40.3	386	1	P90526	B cell stimulating fac	1.55e-106		
16	1368	36.0	182	1	W00403	Interleukin-6 antagoni	1.52e-93		
17	1320	34.7	460	1	R22616	IL-6R for soluble IL-6	8.53e-90		
18	1311	34.5	460	1	R13318	IL-6 receptor.	4.30e-89		
19	1289	33.9	186	1	P80270	Recombinant Interleuki	2.25e-87		
20	1289	33.9	186	1	R75765	Human interleukin-6.	2.25e-87		
21	1287	33.8	184	1	R03914	Polypeptide with human	3.22e-87		
22	1287	33.8	184	1	R55256	Interleukin 6.	3.22e-87		
23	1287	33.8	184	1	P81158	Polypeptide with B-cel	3.22e-87		

ALIGNMENTS

RESULT 1									
ID	W36846	standard; Protein; 525 AA.	184	1	R20783	Interleukin-6.	33.8	1287	3.22e-87
AC	W36846;		184	1	R4990	Mutant Interleukin 6 S	33.8	1287	3.22e-87
DT	25-MAR-1998 (first entry)		184	1	W02609	Interleukin-6.	33.8	1287	3.22e-87
DE	Human fusion polypeptide H-IL-6 with 18 amino acid linker.		184	1	R06532	Human B-cell simulator	33.8	1287	3.22e-87
KW	Interleukin-6; IL-6; Interleukin-6 receptor; IL-6R; ligand; conjugate;		184	1	R06532	B-cell differentiation	33.8	1287	3.22e-87
KW	protein interaction; therapeutic; antagonist.		184	1	R06532	Segment of human B cel	33.8	1287	3.22e-87
OS	Synthetic.		185	1	R05274	Human Interleukin-6 fr	33.8	1287	3.22e-87
OS	Homo sapiens.		185	1	R05275	Segment of human B cel	33.8	1287	3.22e-87
FH	Key	Location/Qualifiers	185	1	R68624	Ala-BCDF.	33.8	1287	3.22e-87
FT	Peptide	1. .19	185	1	R13471	hIL-6 protein.	33.8	1287	3.22e-87
FT	Protein	/label= signal_peptide	188	1	W95011	Human Interleukin-6 (I	33.8	1287	3.22e-87
FT	Region	/note= "H-IL-6 fusion polypeptide"	208	1	P81160	Polypeptide with B-cel	33.8	1287	3.22e-87
FT		/label= linker region	212	1	R05415	Human B-cell different	33.8	1287	3.22e-87
FT		/note= "Links together COOH-terminus of sIL-6R with the NH2-terminus of IL-6"	212	1	P70238	Interferon-beta 2A.	33.8	1287	3.22e-87
PN	WO9732891-A2.		212	1	R72317	Interferon-beta2A.	33.8	1287	3.22e-87
PD	12-SEP-1997.		212	1	R49041	Human Interleukin-6.	33.8	1287	3.22e-87
PF	07-MAR-1997; D00458.		212	1	P90371	pBSF2-L8	33.8	1287	3.22e-87
PR	07-MAR-1996; DE-008813.		212	1	R49249	Sequence of human B-ce	33.8	1287	3.22e-87
PA	(ANGE-) ANGEWANDTE GENTECNOLOGIE SYSTEME GMBH.		212	1	R33430	IFN-beta-2a.	33.8	1287	3.22e-87
PI	Rose-John S;		212	1	R34726	Human IL-6 (for modifi	33.8	1287	3.22e-87
DR	WPI: 97-470536/43.		212	1	P90047	pBSF2-L8 sequence	33.8	1287	3.22e-87
DR	N-PSDB; T97848.		212	1	P90436	Interferon-beta-2.	33.8	1287	3.22e-87
PT	Conjugate of two peptide(s) with mutual affinity connected by a linker - used to modulate interactions between proteins, e.g. for ex vivo expansion of human stem cells								
PS	Disclosure; Fig 1: 19pp; German.								
CC	This sequence represents the fusion polypeptide H-IL-6 which contains an 18 amino acid linker which joins the carboxy terminus of human interleukin-6 receptor (IL-6R) with the amino terminus of human interleukin-6 (IL-6). Such conjugates could be used to modulate interactions between proteins, particularly to overcome interrupted interactions caused by an incomplete interleukin-6 (IL-6) receptor. These constructs derived from IL-6 and its receptor, can also be used for ex vivo expansion of human stem cells, and as a therapeutic IL-6 receptor antagonist.								
CC	Sequence 525 AA;								
Query Match	100.0%;	Score 3803;	DB 1;	Length 525;					
Best Local Similarity	100.0%;	Pred. No. 8.73e-286;							
Matches	525;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Db	1	MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFQVPEDNATVHW 60							

		Best Local Similarity 100.08; Pred. No. 1.55e-174; Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ddb	1 MLAVGCCALLAALAAACGAALAPRCPAQVARGVLTSIPGDSVTLTCPGVPEPNATVHW 60 	
Qy	1 MLAVGCCALLAALAAACGAALAPRCPAQVARGVLTSIPGDSVTLTCPGVPEPNATVHW 60 	
Ddb	61 VLRKPAAGSHPSRWAGNGRRLLRLSRVOLHSDGNYSYCYRAGRPAGTIVHLVDVPPEPQLS 120 	
Qy	61 VLRKPAAGSHPSRWAGNGRRLLRLSRVOLHSDGNYSYCYRAGRPAGTIVHLVDVPPEPQLS 120 	
Ddb	121 CFRKSPLSNVVCEWGRSPSLTTKAULLVRKFONSPAEDFQPCOYSOESOKESCQLAV 180 	
Qy	121 CFRKSPLSNVVCEWGRSPSLTTKAULLVRKFONSPAEDFQPCOYSOESOKESCQLAV 180 	
Ddb	181 PEGDSSFYIYSMCVASSVGSKFSKTFTGCGLQPDPANITTVAYARNPRWLSTWTQD 240 	
Qy	181 PEGDSSFYIYSMCVASSVGSKFSKTFTGCGLQPDPANITTVAYARNPRWLSTWTQD 240 	
Ddb	241 PHSWNSFEYLRIELRYRAERSKITFTTMVKDLQHCHVIHDWSGLRHVQLRAQEFGQ 300 	
Qy	241 PHSWNSFEYLRIELRYRAERSKITFTTMVKDLQHCHVIHDWSGLRHVQLRAQEFGQ 300 	
Ddb	301 GEWSEWPEAMGTPWTESRPPTA 323 	
Qy	301 GEWSEWPEAMGTPWTESRPPTA 323 	
	RESULT 6	
ID	P90284 standard; Protein; 468 AA.	
AC	G90284;	
DE	31-MAR-1992 (first entry)	
DT	Sequence of a receptor protein for human B cell stimulating	
DE	factor-2 (BSf2 receptor).	
KW	B cell; immune disorder; therapy; diagnosis; prophylaxis.	
OS	Homo sapiens.	
FF	Key	Location/Qualifiers
FT	region	2..22
FT	region	/label= hydrophobic region
FT	region	362..386
FT	region	/label= hydrophobic region
PN	EP-325474-A.	
PD	26-JUL-1989.	
PF	20-JAN-1989; 300536.	
PP	22-JAN-1988; JP-012387.	
PR	25-JUN-1988; JP-012599.	
PR	04-AUG-1988; JP-194885.	
PR	14-JAN-1989; JP-017461.	
PR	20-JAN-1989; JP-009774.	
PPA	(KISH/) KISHIMOTO T.	
PI	Kishimoto T;	
DR	WPI; 89-214667/30.	
DR	N-PADB; N90340.	
PPT	Receptor protein for human B cell stimulating factor-2 - obtd. by recombinant DNA techniques and used as diagnostic, prophylactic or therapeutic agent	
PT	Claim 2; Page 19-21; 63pp; English.	
CC	The cDNA in N90340 was derived from monocyte cell line U937.	
CC	Isolated BSf2 receptor and DNA encoding it are claimed, as are	
CC	(b) expression vectors; (c) host organisms; (d) antibodies; and	
CC	(e) hybridomas.	
SC	Sequence 468 AA;	
	Query Match 63.1%; Score 2398; DB 1; Length 468; Best Local Similarity 100.0%; Pred. No. 1.55e-174; Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Ddb	1 MLAVGCCALLAALAAACGAALAPRCPAQVARGVLTSIPGDSVTLTCPGVPEPNATVHW 60 	
Qy	1 MLAVGCCALLAALAAACGAALAPRCPAQVARGVLTSIPGDSVTLTCPGVPEPNATVHW 60 	
Ddb	61 VLRKPAAGSHPSRWAGNGRRLLRLSRVOLHSDGNYSYCYRAGRPAGTIVHLVDVPPEPQLS 120 	

Db	181	PEGSSSYIYVSMCVASSVSGSKFSTQTTFQCGGILQDPPANITVTAVARNPRLSVTWQD	240
Qy	181	PEGSSSYIYVSMCVASSVSGSKFSTQTTFQCGGILQDPPANITVTAVARNPRLSVTWQD	240
Db	241	PHSNSSFYRLRFLRYRAERSKTFTTMMVKDLQHCVCVTHDAWSGLRHVVQLRAQEFQ	300
Qy	241	PHSNSSFYRLRFLRYRAERSKTFTTMMVKDLQHCVCVTHDAWSGLRHVVQLRAQEFQ	300
Db	301	GENSESPAMGTPWTESRPPA	323
Qy	301	GENSESPAMGTPWTESRPPA	323
RESULT 8			
ID	R98364	standard; Protein; 468 AA.	
AC	R98364;		
DT	28-NOV-1996	(first entry)	
DE	Interleukin-6 receptor.		
KW	Interleukin-6; IL; receptor; antisense oligonucleotide; Inhibition;		
KW	gene expression; kidney tumour; myeloma; Kaposi's sarcoma; psoriasis;		
KW	rheumatoid arthritis; endotoxic shock.		
OS	Homo sapiens.		
PN	WO9618416-A1.		
PD	20-JUN-1996.		
PF	15-DEC-1995; J02587.		
PR	16-DEC-1994; JP-313167.		
PR	18-AUG-1995; JP-210739.		
PA	(CHUS) CHUGAI SEIYAKU KK.		
PI	Koishibara Y, Kuromaru K;		
DR	WPL; 96-300392/30.		
DR	N-PSDB; T31441.		
PT	Anti-sense oligo:nucleotide inhibitor against human IL-6R expression		
PT	- for treatment of e.g. tumours, cancers, rheumatoid arthritis,		
PT	psoriasis, endo:toxic shock, etc.		
PS	Claim 2; Page 17-21: 32pp: Japanese.		
CC	Antisense oligonucleotides may be used to inhibit the expression of		
CC	the interleukin-6 receptor. Inhibition of expression of the		
CC	IL-6 receptor is useful in the treatment of kidney tumours, myeloma,		
CC	Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxic		
CC	shock. The antisense oligonucleotides are administered at a dosage		
CC	of 0.1-100mg/kg, pref. 0.1-50 mg/kg.		
SQ	Sequence 468 AA;		
Query Match 62.9%; Score 2392; DB 1; Length 468;			
Best Local Similarity 99.7%; Pred. No. 4.62e-174;			
Matches 322; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Db	1	MLAVGCALLAALAAAPCAALAPRCAPAEVARGVLISLPGDSVTLTCPGVEPEDNATVHW	60
Qy	1	MLAVGCALLAALAAAPCAALAPRCAPAEVARGVLISLPGDSVTLTCPGVEPEDNATVHW	60
Db	61	LLRKPAGSHPSRWAGMGRLLRSVOLHDSGNVSCYRAGRAGTVHLLVDVPPPEPQLS	120
Qy	61	LLRKPAGSHPSRWAGMGRLLRSVOLHDSGNVSCYRAGRAGTVHLLVDVPPPEPQLS	120
Db	121	CFRKPSLSNVVCEWGPRTSLTKAVLLVRKFQNSPAEDFQPCQYSOESQKFSQQLAV	180
Qy	121	CFRKPSLSNVVCEWGPRTSLTKAVLLVRKFQNSPAEDFQPCQYSOESQKFSQQLAV	180
Db	181	PEGSSSYIYVSMCVASSVSGSKFSTQTTFQCGGILQDPPANITVTAVARNPRLSVTWQD	240
Qy	181	PEGSSSYIYVSMCVASSVSGSKFSTQTTFQCGGILQDPPANITVTAVARNPRLSVTWQD	240
Db	241	PHSNSSFYRLRFLRYRAERSKTFTTMMVKDLQHCVCVTHDAWSGLRHVVQLRAQEFQ	300
Qy	241	PHSNSSFYRLRFLRYRAERSKTFTTMMVKDLQHCVCVTHDAWSGLRHVVQLRAQEFQ	300
Db	301	GENSESPAMGTPWTESRPPA	323
Qy	301	GENSESPAMGTPWTESRPPA	323

DB 301 GEWSESPAMGTPWTSRSPPA 323
 QY 301 GEWSESPAMGTPWTSRSPPA 323

RESULT 10
 ID P90525 standard; protein; 468 AA.
 AC P90525;
 DT 23-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 DE B cell stimulating factor-2 receptor; monocyte U937 cell line.
 KW Homo sapiens.
 OS Homo sapiens.
 PN AU8928720-A.
 PD 27-JUL-1989.
 PF 23-JAN-1989; 28720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadimitsu Kishimoto.
 PI Kishimoto T;
 DR WPI; 89-264012/37.
 DR N-PSDB; P90525.
 DT Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders.
 PS Claim 2; page 36; 76pp; english.
 CC The BSF2 receptor is derived from a monocyte U937 cell line. It can be
 CC used to develop prophylactic and therapeutic pharmaceuticals, as agents to
 CC relate diseases and disorders to abnormal BSF-2 prodn. It can also be
 CC used to study an immune mechanism with which BSF-2 or the receptor is
 CC concerned. 468 AA;
 SQ Sequence 468 AA;

Query Match 62.8%; Score 2390; DB 1; Length 468;
 Best Local Similarity 99.7%; Pred. No. 6.65e-174;
 Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MLAVGCALLAALAPGALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPEDNATVHW 60
 QY 1 MLAVGCALLAALAPGALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPEDNATVHW 60
 DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 DB 121 CFRKPSLNNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 QY 121 CFRKPSLNNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 DB 181 PGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 QY 181 PGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWGLRHVVQLRAQEEFGQ 300
 QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWGLRHVVQLRAQEEFGQ 300
 DB 301 GEWSESPAMGTPWTSRSPPA 323
 QY 301 GEWSESPAMGTPWTSRSPPA 323

RESULT 11
 ID W71371 standard; Protein; 468 AA.
 AC W71371;
 DT 02-FEB-1999 (first entry)
 DE Human interleukin-6 receptor alpha polypeptide.
 DE Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;
 KW therapy.
 OS Homo sapiens.
 PN W09835694-A2.

PD 20-AUG-1998.
 PF 10-FEB-1998; U08998.
 PR 11-FEB-1997; US-795473.
 PA (DAVI/) DAVIDSON C M.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 DR WPI; 98-520755/44.
 PT Treatment of hepatitis B virus infection - using a soluble active
 PT agent which prevents interaction of HBV with hepatocytes mediated by
 PT human Interleukin 6
 PS Disclosure; Fig 9; 51pp; English.
 CC This is a previously reported amino acid sequence for human
 CC Interleukin-6 (hIL-6) receptor alpha. The invention relates to
 CC the finding that hIL-6 is essential for hepatitis B virus (HBV)
 CC infection. The invention provides a pharmaceutical composition for
 CC the treatment of HBV infection, comprising a soluble active agent
 CC that interacts with at least one of the binding sites between hIL-6
 CC and the pSI region of HBV and between hIL-6 and hepatocytes and
 CC other HBV-permissive cells. The active agent competitively binds
 CC to at least one of these sites and thereby prevents hIL-6-mediated
 CC HBV infection of hepatocytes and other HBV-permissive cells. The
 CC soluble active agent is selected from glycoprotein 80 (gp80) having
 CC receptor sites which interact with hIL-6, soluble glycoprotein 130
 CC (gp130) having receptor sites which interact with hIL-6, hIL-6
 CC derived peptide Lys41-Ala56, hIL-6 derived peptide Gly77-Glu95,
 CC hIL-6 derived peptide Gln153-His165, a combined 1 and 2 hIL-6,
 CC mutant (mhIL-6 1+2), and mhIL-6 1+2 substituted with Phe171 to Leu
 CC and Ser177 to Arg, and mixtures of any of these.
 CC Sequence 468 AA;
 SQ Sequence 468 AA;

Query Match 62.4%; Score 2373; DB 1; Length 468;
 Best Local Similarity 99.1%; Pred. No. 1.46e-172;
 Matches 320; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 1 MLAVGCALLAALAPGALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPEDNATVHW 60
 QY 1 MLAVGCALLAALAPGALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPEDNATVHW 60
 DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 DB 121 CFRKPSLNNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 QY 121 CFRKPSLNNVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 DB 181 PGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 QY 181 PGDSSFYIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVAVARNPRLSVTWQD 240
 DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWGLRHVVQLRAQEEFGQ 300
 QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWGLRHVVQLRAQEEFGQ 300
 DB 301 GEWSESPAMGTPWTSRSPPA 323
 QY 301 GEWSESPAMGTPWTSRSPPA 323

RESULT 12
 ID P90527 standard; protein; 323 AA.
 AC P90527;
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 DE B cell stimulating factor-2 receptor; monocyte U937 cell line.
 KW Homo sapiens.
 OS Homo sapiens.
 PN AU8928720-A.
 PD 27-JUL-1989.
 PF 23-JAN-1989; 28720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadimitsu Kishimoto.

PI Kishimoto T;
DR WPI; 89-264012/37.
DR N-PSDB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Claim 6; page 39; 76pp; english.
CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocytic U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate
CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
CC study an immune mechanism with which BSF-2 or the receptor is concerned.
SQ Sequence 323 AA;

Query Match 61.8%; Score 2351; DB 1; Length 323;
Best Local Similarity 98.8%; Pred. No. 7 97e-171;
Matches 318; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1 MLAVGALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Qy 1 MLAVGALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Qy 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSCLAV 180
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSCLAV 180
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIQLPDPANITVTAVARNRWLSVTWQD 240
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIQLPDPANITVTAVARNRWLSVTWQD 240
Db 241 PHSWNSFYRLRFELRYRAERSKTTTWMVKDLQHHCVIHDWSGLRHVVQLRAQEFGQ 300
Qy 241 PHSWNSFYRLRFELRYRAERSKTTTWMVKDLQHHCVIHDWSGLRHVVQLRAQEFGQ 300
Db 301 GEMSEWSPAMGTPWTSRSP 322
Qy 301 GEMSEWSPAMGTPWTSRSP 322

RESULT 13
ID W70805;
AC W70805;
DT 03-FEB-1999 (first entry)
DE Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
OS Synthetic.
FH Key Location/Qualifiers
FT Protein 1..313
FT /note= "truncated interleukin (IL)-6R-alpha domain"
PN US5844099-A.
PD 01-DEC-1998.
PE 27-NOV-1995; 563105.
PR 27-NOV-1995; US-563105.
PR 27-OCT-1993; US-140222.
FA (REGG-) REGENERON PHARM INC.
FI Economides A, Stahl N, Yancopoulos GD;
DR WPI; 99-044669/04.
PT Cytokine antagonists - comprising extracellular domains of
PT specificity-determining and signal-transducing components of
PT cytokine receptor
PS Example 4; Fig 16; 46pp; English.
CC The present sequence represents the amino acid sequence of interleukin
CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
CC invention. The specification describes cytokine antagonists comprising
CC only the extracellular domain of the specificity-determining component of
CC the cytokine receptor and the extracellular domain of a
CC signal-transducing component of the cytokine receptor. The cytokine

is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
granulocyte macrophage colony-stimulating factor (GM-CSF),
gamma-interferon or transforming growth factor-beta (TGF-beta). The
antagonist is capable of binding the cytokine to form a nonfunctional
complex. The compounds have therapeutic activity as cytokine antagonists
and can also be used in assays for identifying novel agonists and
antagonists of cytokines.
SQ Sequence 315 AA;

Query Match 60.9%; Score 2317; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 3.85e-168;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1 MVAVGALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Qy 1 MLAVGALLAALLAAGAALAPRRCPADEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Qy 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSCLAV 180
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFQNSPAEDFOEPCQYSOESQKFSCLAV 180
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIQLPDPANITVTAVARNRWLSVTWQD 240
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIQLPDPANITVTAVARNRWLSVTWQD 240
Db 241 PHSWNSFYRLRFELRYRAERSKTTTWMVKDLQHHCVIHDWSGLRHVVQLRAQEFGQ 300
Qy 241 PHSWNSFYRLRFELRYRAERSKTTTWMVKDLQHHCVIHDWSGLRHVVQLRAQEFGQ 300
Db 301 GEMSEWSPAMGTP 313
Qy 301 GEMSEWSPAMGTP 313

RESULT 14
ID R70122 standard; Protein; 1042 AA.
AC R70122;
DT 14-FEB-1996 (first entry)
DE IL8-R type 1-GBP 130 fusion protein.
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;
KW GBP 130; GBPH; glycoprotein binding peptide homologue; glycoprotein A.
OS Chimeric Homo sapiens.
OS Chimeric Plasmodium falciparum.
FH Key Location/Qualifiers
FT misc_difference 54
FT /label= OTHER
FT /note= "Arn (sic)"
PN WO9506737-A.
PD 09-MAR-1995.
PF 01-SEP-1994; G01900.
PR 03-SEP-1993; GB-018350.
PR 23-AUG-1994; GB-017021.
PA (PREN/) PRENDERGAST K F.
PI Prendergast RF;
DR WPI; 95-115452/15.
PT New hybrid peptide(s) for binding cytokine(s) - comprising a
PT malaria parasite peptide capable of binding a red blood cell and
PT a receptor peptide.
PS Example A; Page 77-78; 93pp; English.
CC Hybrid peptides for binding cytokines, comprising a malaria parasite
CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC of these hybrid peptides. R70122 is a fusion of interleukin 6 receptor
CC (as confirmed with reference to SWISSPROT, as it is unclear in the
CC specification whether this sequence is IL6-R or IL8-R type) and
CC glycoprotein binding protein (GBP) 130. The use of cytokine receptors not
CC normally found on RBCs means that the cytokine can bind harmlessly to the
CC RBC without deleterious effect. The RBC protects the hybrid peptides from

CC excretion from the kidney, and due to steric hindrance prevents the
CC cytokines binding to a receptor in another cell. GBP 130 or GBPH
CC (GBP homologue) are the pref. malaria parasite peptides used, others
CC include EBA 175 (175 kDa erythrocyte binding antigen), PMSA (pre major
CC merozoite surface antigen) and the Duffy binding receptor molecule (eg.
CC exhibited by Plasmodium vivax). These peptides bind to pref. glycophorin
CC A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid
CC peptides are thus used to lower the levels of free cytokines in the
CC circulation to reduce pathological damage.
SQ Sequence 1042 AA;

Query Match 55.5%; Score 2110; DB 1; Length 1042;
Best Local Similarity 97.0%; Pred. No. 8.14e-152;
Matches 295; Conservative 0; Mismatches 1; Indels 8; Gaps 2;

Db 1 LAPRCFAQEVARGVLTSLPGDSTVLTCPGVEPDNATVHVLKPAAGSHPSXWAGMR 60
QY 20 LAPRCFAQEVARGVLTSLPGDSTVLTCPGVEPDNATVHVLKPAAGSHPSXWAGMR 79
Db 61 RLLRSVQLHDSGNYSY-AGRAGTIVHLLVDVPPPEPQLSCFRKSPLSNVVCEWGPRT 119
QY 80 RLLRSVQLHDSGNYSYRAGRAGTIVHLLVDVPPPEPQLSCFRKSPLSNVVCEWGPRT 139
Db 120 PSLTTKAVLLVRKFQNSPAEDFQE-----SOKFSQCLAVPEGDSFSFYIVSMCVASSVG 172
QY 140 PSLTTKAVLLVRKFQNSPAEDFQEPCOYSQESQKFSQCLAVPEGDSFSFYIVSMCVASSVG 199
Db 173 SKFSKTQTFQCGGTLQDPDPANITVAVARNPRLSVTWQDPHSWNSFFRLRFLRYRA 232
QY 200 SKFSKTQTFQCGGTLQDPDPANITVAVARNPRLSVTWQDPHSWNSFFRLRFLRYRA 259
Db 233 ERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPAMGTPWTESR 292
QY 260 ERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPAMGTPWTESR 319
Db 293 SPPA 296
QY 320 SPPA 323

RESULT 15
ID P90526 standard; protein; 386 AA.

AC P90526;
DT 25-JAN-1990 (first entry)
DE B cell stimulating factor-2 receptor.
KW B cell stimulating factor-2 receptor; monocyte U937 cell line.
OS Homo sapiens.
PN AU8928720-A.
PD 27-JUL-1989.
PF 23-JAN-1989; 28720.
PR 22-JAN-1988; JP-012387.
PR 25-JAN-1988; JP-012599.
PR 04-AUG-1988; JP-194885.
PR 14-JAN-1989; JP-007461.
PA (KISH) Tadamoto Kishimoto.
PI Kishimoto T;
DR WPI; 89-264012/37.
DR N-PSDB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Claim 4; page 37-8; 76pp; english.
CC The BSF2 receptor has residues near the N-terminal deleted. The receptor
CC is derived from a monocyte U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals as agents to relate diseases
CC and disorders to abnormal BSF-2 prodn. It can also be used to study an
CC immune mechanism with which BSF-2 or the receptor is concerned.
SQ Sequence 386 AA;

Query Match 40.3%; Score 1534; DB 1; Length 386;
Best Local Similarity 97.7%; Pred. No. 1.55e-106;
Matches 211; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

Db 28 VDVPPPEPQLSCFRKSPLSNVVVC--GPRSTPMSLTTKAVLLVRKFQNSPAEDFQEPCOY 85
QY 110 VDVPPPEPQLSCFRKSPLSNVVCEWGPRT--SLTTKAVLLVRKFQNSPAEDFQEPCOY 167
Db 86 SQESQKFSQCLAVPEGDSFSFYIVSMCVASSVGSKFSKTQTFQCGGTLQDPDPANITVAV 145
QY 168 SQESQKFSQCLAVPEGDSFSFYIVSMCVASSVGSKFSKTQTFQCGGTLQDPDPANITVAV 227
Db 146 ARNPRWLSVTWQDPHSWNSFFRLRFLRYRAERSKFTTMMVKDLQHCVIHDAWSGLR 205
QY 228 ARNPRWLSVTWQDPHSWNSFFRLRFLRYRAERSKFTTMMVKDLQHCVIHDAWSGLR 287
Db 206 HVVOLRAQEEFGQGEWSEWSPAMGTPWTESRPPA 241
QY 288 HVVOLRAQEEFGQGEWSEWSPAMGTPWTESRPPA 323

Search completed: Thu Aug 10 16:00:00 2000
Job time : 60 secs.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2000, 05:41:00 ; Search time 1178.81 Seconds
(without alignments)
6030.355 Million cell updates/sec

Title: US-09-142-471-3
Perfect score: 1612
Sequence: 1 gtcgacgcatgagtgtag.....gtacatgggcaccgtcgac 1612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues
Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: gb_est30:*
50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: em_est35:*
83: em_est36:*
84: em_est37:*
85: gb_est48:*
86: gb_est49:*
87: gb_est50:*
88: gb_est51:*
89: gb_est52:*
90: gb_est53:*
91: gb_est54:*
92: gb_est55:*
93: gb_gss1:*
94: gb_gss2:*
95: gb_gss3:*
96: gb_gss4:*
97: em_gss1:*
98: em_gss2:*
99: em_gss3:*
100: em_gss4:*
101: gb_gss5:*
102: gb_gss6:*
103: gb_gss7:*
104: gb_gss8:*
105: gb_gss9:*
106: em_gss5:*
107: em_gss6:*
108: em_gss7:*
109: em_gss8:*
110: em_gss9:*
111: em_gss10:*
112: em_gss11:*
113: gb_gss10:*
114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*

QY	1162	aaggagacatgtacaagaagtaacatgtgtgaagaagcagcaagaagagcactgcgcagaaac	1221
Db	264	AAGGAGACATGTAAACAGAGTAACTGTGTGAAGCAGCAAGAGAGCCTGGCAGAAAC	323
QY	1222	aacctgaacctccaagatggcct-gaaaaagatgagtgcttcccaatctggaatcaatga	1280
Db	324	AACCTGAACCTTCCAAGATGGCTCGAAAAGATGGATGCTTCCANTCTGGATTCATGA	383
QY	1281	ggagacttgctggtgaaatcatcac-tggctcttttgagtttgaggtataccttagagt	1339
Db	384	GGAGACTTGCTGGTGAATAATCATCTACTTGGCTTTTGGAGTTTCAGCTATACCTAGAGT	443
QY	1340	acctcagaacacagatttgagtag-tgaggaaacagccagagctgtgcagatagataga	1398
Db	444	ACCTCCAGAACAGATTTGAGTAGTTGAGGAAACAAAGCCAGAGCTGTGCAGATGAGTACA	503
QY	1399	aagttctgtatccagtttctcgcagaaaaagcagaagaatctagatgcaataaccacccc-	1457
Db	504	AAGTCTTGATCCAGTTCCTTTCAGAAAAAGGCAAGATCTAGATGCNATNACCACCCCT	563
QY	1458	tgaccccaaccacaaatgccagcctgctgacga	1489
Db	564	TGACCCCAACCACAATGCCAGCCTGCTGACGA	595
RESULT 3			
AI751501			
LOCUS	AI751501	481 bp	mRNA
DEFINITION	cn10c12.y1 Normal Human Trabecular Bone Cells EST	22-JUN-1999	
ACCESSION	clone NHTBC_cnl0c12	random, mRNA sequence.	
VERSION	AI751501		
KEYWORDS	AI751501.1	GI:5129765	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 481)		
JOURNAL	Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.		
COMMENT	SCAP: The Skeletal Genome Anatomy Project		
	Unpublished (1997)		
	On Jun 22, 1998 this sequence version replaced gi:3247051.		
	Contact: Libin Jia		
	National Human Genome Research Institute		
	10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA		
	Tel: 301-402-4877		
	Fax: 301-496-7157		
	Email: libin@helix.nih.gov		
	DNA Sequencing and Analyses by National Institutes of Health Intramural Sequencing Center (NISC).		
	Plate: 10 row: c column: 12		
	Seq primer: M13RPI reverse primer (ABI).		
FEATURES	Location/Qualifiers		
source	1. .481		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="NHTBC_cnl0c12"		
	/clone_lib="Normal Human Trabecular Bone Cells"		
	/sex="Female"		
	/tissue_type="Bone"		
	/cell_type="Trabecular Bone Cells"		
	/lab_host="SURE"		
	/note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI"		
BASE COUNT	137 a 131 c 112 g 101 t		
ORIGIN			
Query Match	22.6%	Score 364;	DB 43; Length 481;
Best Local Similarity	100.0%;	Pred. No. 4.2e-86;	
Matches 364;	Conservative 0;	Mismatches 0;	Indels 0; Gaps

Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagan, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Hasetline, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence

Nature 377, 3-174 (1995)

JOURNAL 96026280

MEDLINE

COMMENT

On Dec 20, 1995 this sequence version replaced gi:1135864.

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)

Insert Length: 716 Std Error: 0.00

Seq primer: M13 Reverse

High quality sequence stop: 92.

FEATURES

source

1. .287

/organism="Homo sapiens"

/db_xref="ATCC (inhost):105671"

/db_xref="taxon:9606"

/clone_lib="Human Bone"

/tissue_type="bone"

BASE COUNT 81 a 69 c 65 t 4 others

ORIGIN

Query Match 15.4%; Score 248.6; DB 89; Length 287;

Best Local Similarity 96.9%; Pred. No. 1.6e-55;

Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1353 atttgagtagtagtggagcaaacgacagctgtgcagatgagtagcaaaagtcttgatcca 1412

|||||

Db 1 ATTTGAGAGTAGTGAGGAACCAAGCCAGAGCTGTGCAGATGAGTACAAAATTCCTGATCCA 60

|||||

QY 1413 gtctctgcagaaaagcgaagaatctagatgcaataaccacctgaccccaaccacaaa 1472

|||||

Db 61 NTTCTCGAGNAAAGGCAGAGANTCTAGATGCAATACCAACCCCTGACCCCAACCAAAA 120

|||||

QY 1473 tgcagcctgtgcagagctgtgcagagacacagctggctgcagagatgacaaactca 1532

|||||

Db 121 TGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCACTGCTGCAGGACATGACAACTCA 180

|||||

QY 1533 tctaatctgcagagctttaagagattctctgcagctcagcagctgagggctcttcggcaaat 1592

|||||

Db 181 TCTCATTTCTGCGCAGTTTAAAGGAGTTCTGACAGTCCAGCTGAGGGCTCTTCGGCAAAAT 240

|||||

QY 1593 gtacatgggacacgctcga 1611

|||||

Db 241 GTAGCATGGGCACCTCAGA 259

|||||

RESULT 8

AI472218/c 655 bp mRNA EST 14-APR-1999

LOCUS

DEFINITION tJ86e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148410 3' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI472218

VERSION AI472218.1 GI:4334308

KEYWORDS EST.

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 655)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT On May 18, 1998 this sequence version replaced gi:3138589.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 709 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 444.

FEATURES

source

1. .655

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pTT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaudo."

BASE COUNT 201 a 125 c 113 g 213 t 3 others

ORIGIN

Query Match 14.9%; Score 240.2; DB 40; Length 655;

Best Local Similarity 97.6%; Pred. No. 3.4e-53;

Matches 242; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1364 gtgaggcaaacgacagagctgtgcagatgagtagcaaaagtctcagttcctcgaga 1423

|||||

Db 655 GTGAGGCAACAGCCAGAGCTGTGCAGATGAGTACAAAAGTCNTGATCCAGTCTCTGCAGA 596

|||||

QY 1424 aaaggcaagaatctagatgcaataaccacctgaccccaaccacacacagcctgc 1483

|||||

Db 595 AAAAGGCAAGAATCTAGATGCAATACCAACCCCTGACCCCAACCAACNATGCCAGCTGC 536

|||||

QY 1484 tgacgaagctgcaggcacagacacagctggctgcaggagcatgacaaactcatctctgc 1543

|||||

Db 535 TGACGAAGCTGCAGCACAGAACCACTGGCTGCAGGACATGACAACTCATCTCATTTCTGC 476

|||||

QY 1544 gcagcttaaggagttcctcagtcagtcagcctcgagggctcttcgcgcaaatgtagcatgggc 1603

|||||

Db 475 GCAGCTTTAAGGAGTTCTGCACTCCAGCTGAGGGCTCTTCGGCAAAATGTAGCATGGGC 416

|||||

QY 1604 accgtca 1611

|||||

Db 415 ACCTCAGA 408

|||||

[illegible]

Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018698056
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES	source
Location/Qualifiers	
1. .280	
/organism="Homo sapiens"	
/db_xref="ATCC (inhost):185955"	
/db_xref="taxon:9606"	
/clone_lib="Activated T-cells I"	
/cell_type="T-lymphocyte"	
/dev_stage="adult"	
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"	
BASE COUNT	93 a 62 c 67 g 58 t

	Query Match	13.4%;	Score 216.4;	DB 25;	Length 280;
	Best Local Similarity	99.5%;	Pred. No. 5.6e-47;		
	Matches 217;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0
Qy 1166	agacatgtaacaagagtaa	cattgtgaaagcagcaagaagaggaactggcgcaaaaacacc	1225		
Db 63	AACATGTAAACAAGATTAACATGTTGAAGACGCCAAGAAGAGCACTGGCAGAAAAACACC	122			
Qy 1226	tgaaccttccaaagatgctgtgaaaaagatgatcttcctaacttgattcaatgaggaga	1285			
Db 123	TGAACCTTCCAAAGATGCTGAAAAGATGATGCTTCCAATCTGGATTCAATAGAGAGA	182			
Qy 1286	cttgcctgggtgaaaatacatcactgctcttttggagttaggattacacctagaqtagctgcc	1345			

```

|||||
Db 183 CTTGCCCTGGTGAATAATCATCTCGTCTTTTGGAGTTTGAGGTATACCTAGTACCTCC 242
|||||

Qy 1346 aaacacagatttgagtagtgaggaacaacacagcagct 1383
|||||
Db 243 AGACACAGATTTCAGAGTAGTGAGGACCAAGCCAGACCT 280
|||||

RESULT 10
W51812
LOCUS
DEFINITION
W51812.1 618 bp mRNA EST 11-OCT-1996
clone IMAGE:325591 5' similar to gb:X04430 INTERLEUKIN-6 PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 618)
Hillier L., Clark N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, F., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
On Apr 7, 1998 this sequence version replaced gi:3036007.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 733 Std Error: 0.00
Seq primer: ETPRimer
High quality sequence stop: 493.

```

```

FEATURES
source
1. .618
location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:1257103"
/db_xref="taxon:9606"
/clone="IMAGE:325591"
/clone_lib="Soares senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT7T3D (Pharmacia) with a modified
polylinker V.TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'.
TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
185 a 109 c 121 g 192 t 11 others
BASE COUNT
ORIGIN

```

Query Match	13.08;	Score 210;	DB 91;	Length 618;
Best Local Similarity	96.8%;	Pred. No. 3.5e-45;		
Matches 213;	Conservative	0;	Mismatches 7;	Indels 0; Gaps 0;
QY	1392	gagtcacaaagtcctgattccagttcctgcagaaaaagcgaagaatactagatgcaataac	1451	
Db	13	GGGTACAAAAGTCTGTATCCAGTTCCTGCAGAAAAGGCAAAAGAAATCTAGATGCAATANC	72	

```

QY 1452 caccctgacccacacacaaatgcagcctgctgacgaagctgcagcagcacagaccagtg 1511
      |||||||
Db 73 CACCCCTGACCCACACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCCAGT 132

QY 1512 gctgcaggacatgacaaactcatctcattctgcgcagctttaagaggttcttcgagtcag 1571
      |||||||
Db 133 GCTGCAGGACATGACAACTCATCTCATCTCGCGCANTTTTAAAGGAGTTCCTGCGAGTCCAG 192

QY 1572 cctgcaggctcttcgcaaatgtagcggccaccgctcga 1611
      |||||||
Db 193 CCTGAGGCGCTCTTCGGCAATGTAGCATGGGCACCTCAGA 232

RESULT 11
AA381892
LOCUS AA381892 311 bp mRNA EST 21-APR-1997
DEFINITION EST95205 Activated T-cells I Homo sapiens cDNA 5' end similar to
      interleukin 6, mRNA sequence.
ACCESSION AA381892
VERSION AA381892
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
      Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
      White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
      Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
      Fitzgerald,L.M., Fitchugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
      Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
      Kelley,J.M., Kelley,J.F., McDonald,L.A., Marmaros,S.M., Merrick,J.M.,
      Moreno-Palauques,R.F., Nguyen,D.T., Pelligrino,S.M.,
      Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
      Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
      Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
      Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
      He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
      Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
      Raymond,L.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
      Fraser,C.M. and Venter,J.C.
      Initial assessment of human gene diversity and expression patterns
      based upon 83 million nucleotides of cDNA sequence
      Nature 377 (6547 Suppl), 3-174 (1995)
      12140200
      Other_ESTs: THC167228
      Contact: Kerlavage, AR
      Bioinformatics
      The Institute for Genomic Research
      9712 Medical Center Drive, Rockville, MD 20850 USA
      Tel: 3018699056
      Fax: 3018699423
      Email: arkerlavet@tigr.org
      For clone availability, additional sequence and expression
      information related to this EST, please check the TIGR Human Gene
      Index (http://www.tigr.org/tdb/hgi/hgi.html)
      Seq primer: M13 Reverse.
      Location/Qualifiers
      1. .311
         /organism="Homo sapiens"
         /db_xref="ATCC (inhost):186438"
         /db_xref="taxon:9606"
         /clone_lib="Activated T-cells I"
         /cell_type="T-lymphocyte"
         /dev_stage="adult"
         /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
         XhoI"
BASE COUNT 86 a 99 c 68 g 58 t
ORIGIN

```

```

Query Match 11.5%; Score 186; DB 25; Length 311;
Best Local Similarity 100.0%; Pred. No. 6.8e-39;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1042 ccagtagcccccagagagattccaaagatgtagccgcccccacacagaccactcacc 1101
      |||||||
Db 126 CCAGTAGCCCCAGAGAGAGATTTCAAAAGATGTAGCCGCCGCCACACAGACGCCACTCACC 185

QY 1102 tcttcagaacgaattgacaaacaaattcgttacatctcctcaagcctatcagccctcaga 1161
      |||||||
Db 186 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCTCGACGCCGATCTCAGCCCTGAGA 245

QY 1162 aaggagacatgtaacaagagtaacatgtgtgaagcagcaagaagcactgcgagaaaaa 1221
      |||||||
Db 246 AAGGAGACATGTACAAGAGTAACATGTGTGAAGACGACGAAGGCGACTGCGAGAAAAC 305

QY 1222 aacctg 1227
      |||||||
Db 306 AACCTG 311

RESULT 12
AA380919
LOCUS AA380919 316 bp mRNA EST 21-APR-1997
DEFINITION EST93950 Activated T-cells V Homo sapiens cDNA 5' end similar to
      interleukin 6, mRNA sequence.
ACCESSION AA380919
VERSION AA380919.1 GI:2033259
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
      Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
      White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
      Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
      Fitzgerald,L.M., Fitchugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
      Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
      Kelley,J.M., Kelley,J.F., McDonald,L.A., Marmaros,S.M., Merrick,J.M.,
      Moreno-Palauques,R.F., Nguyen,D.T., Pelligrino,S.M.,
      Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
      Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
      Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
      Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
      He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
      Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
      Raymond,L.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
      Fraser,C.M. and Venter,J.C.
      Initial assessment of human gene diversity and expression patterns
      based upon 83 million nucleotides of cDNA sequence
      Nature 377 (6547 Suppl), 3-174 (1995)
      12140200
      Other_ESTs: THC167228
      Contact: Kerlavage, AR
      Bioinformatics
      The Institute for Genomic Research
      9712 Medical Center Drive, Rockville, MD 20850 USA
      Tel: 3018699056
      Fax: 3018699423
      Email: arkerlavet@tigr.org
      For clone availability, additional sequence and expression
      information related to this EST, please check the TIGR Human Gene
      Index (http://www.tigr.org/tdb/hgi/hgi.html)
      Seq primer: M13 Reverse.
      Location/Qualifiers
      1. .316
         /organism="Homo sapiens"
         /db_xref="ATCC (inhost):185336"
         /db_xref="taxon:9606"
         /clone_lib="Activated T-cells V"
FEATURES
      source

```



```
Query Match          9.2%; Score 148.2; DB 79; Length 311;
Best Local Similarity 96.4%; Pred. No. 7.4e-29;
Matches 161; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1042 ccagtaacccagagagattccaaagatgtatgagcccccacacagagccactcacc 1101
Db 138 CCAGTACCCCGAGAGAGATTCAAAGATGTAGCCGCCCCACACAGACGCCACTCACC 197
QY 1102 tctcagaagaattgacaacaaattcggtacatctcgacgcacatctcagccctgaga 1161
Db 198 TCTTCAGAACGAANTGACAAACATNTCGGTACCTCTCGACGGCATCTCAGCCCTGAGA 257
QY 1162 aaggagacatgtaacaaagatgaaca-tgtgtgaagcagcaaaagag 1207
Db 258 AAGGAGACATGTAAACANGAGTAGCATGTGTGAAAGCAGCAAGAGG 304

RESULT 15
AI982185 628 bp mRNA EST 15-SEP-1999
LOCUS pat.pk0076.f2.f chicken activated T cell cDNA Gallus gallus cDNA
DEFINITION clone.pat.pk0076.f2.f 5' similar to interleukin-6, mRNA sequence.
ACCESSION AI982185
VERSION AI982185.1 GI:5885213
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 628)
AUTHORS Tirunaguru.V.G., Sofer,L. and Burnside,J.
TITLE An expressed-sequence-tag database of activated chicken T cells:
sequence analysis of 5596 clones
JOURNAL Unpublished (1999)
COMMENT On Jun 22, 1998 this sequence version replaced gi:3247580.
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302 831-3651
Email: joan@udel.edu
Seq primer: T7.
FEATURES             Location/Qualifiers
     source            1..628
                        /organism="Gallus gallus"
                        /db_xref="taxon:9031"
                        /clone="pat.pk0076.f2.f"
                        /clone_lib="chicken activated T cell cDNA"
                        /sex="male"
                        /cell_type="Con A-activated splenic T cell"
                        /lab_host="E.coli TOP10 F'"
                        /note="Vector: pCDNA3"
BASE COUNT          152 a 170 c 177 g 128 t 1 others
ORIGIN
```

```
Db 165 GAGGACGGCTGCCTGCTCGCGGGCTTCGACGAGGAGAAATGCCTGACGAACTCTCCAGC 224
QY 1309 ggctcttttgaggtttgaggtatcacctagtagtacctccagaaacagatttgagagtagtgag 1368
Db 225 GGCCTGTTTCGGCTTTCAGACCTACCTGGAATTCATTCAAGAGACTTTTCGATAGGCGAANAAG 284
QY 1369 gaacaagccagagagctgtgcagatgagtacaaaaagtcctgatccagttcctgcagaaaaaag 1428
Db 285 CAGAACGTCGAGTCTCTGTGCTACAGCACAAAGCACCTGGGGGCCACGATCCGGCAGATG 344
QY 1429 gcaagaatctagatgcaataaacacacccctgaccccaaccacaataatgcagcctgctgacg 1488
Db 345 GTGATAAATCCCGATGAAGTGTGTCATCCAGACTCGGGCCGCCAGAAATCCTCTCTCGCC 404
QY 1489 aagctgcaggcacagaaacacagtgctgcagagacatgacaaactcatctcttcgcagc 1548
Db 405 AATCTGAAGTCAGATAAGGACTGGATAGAGAAATACCAATGACCTCATCTCTCCGAGAC 464
QY 1549 ttaagggagttcctgcagtcacagcctgagggctcttcggcaaatgta 1595
Db 465 TTTACTTCGTTTATGGAGAGACCGTGGGGCCGTTGCTACTATTGAA 511

Search completed: August 9, 2000, 05:41:10
Job time: 61707 sec
```

```
Query Match          8.6%; Score 139; DB 47; Length 628;
Best Local Similarity 56.1%; Pred. No. 2.5e-26;
Matches 262; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1129 cggatcacctcagcgcacatcgagccctgagaagagagacatgtaacaagatgaacatg 1188
Db 45 CGGTGCTGCGCGACCGCGCCGTCGACGTCGAGACGAGATGTGCAAGAAGTTCACCGTG 104
QY 1189 tgtgaagcagcaagaggcactggcagcaaaacacacaccttccaaagatggctgaa 1248
Db 105 TGGGAGAACAGCATGGAGATGCTCGTCCGGACAAACCTCAACCTGCCCAAGGTGACGGAG 164
QY 1249 aaagatggatgcttccaatgattcaatgagagagacttgccttggtgaaatcatcact 1308
Db 1249 aaagatggatgcttccaatgattcaatgagagagacttgccttggtgaaatcatcact 1308
```

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	995	61.7	2061	7	5171840-1	Patent No. 5171840
2	995	61.7	2061	7	5480796-1	Patent No. 5480796
3	969	60.1	1074	3	US-08-627-151A-15	Sequence 15, Appl
4	969	60.1	1404	7	5171840-8	Patent No. 5171840
5	969	60.1	1404	7	5480796-8	Patent No. 5480796
6	563.6	35.0	1145	7	5510472-1	Patent No. 5510472
7	551.8	34.2	555	1	US-08-437-680A-1	Sequence 1, Appl
8	550.4	34.1	561	1	US-07-745-382-19	Sequence 19, Appl
9	550.4	34.1	561	1	US-07-921-848-19	Sequence 19, Appl
10	550.4	34.1	561	1	US-08-165-301A-19	Sequence 19, Appl
11	550.4	34.1	561	6	PCR-US94-14179-19	Sequence 19, Appl
12	538.6	33.4	951	5	US-08-469-318-57	Sequence 57, Appl
13	538.6	33.4	951	6	PCR-US95-01185-57	Sequence 57, Appl
14	538.4	33.4	540	6	PCR-US94-12873-3	Sequence 3, Appl
15	535.8	33.2	555	2	US-08-567-047-1	Sequence 1, Appl
16	535.8	33.2	555	3	US-08-567-048-1	Sequence 1, Appl
17	531.2	33.0	561	5	US-08-469-318-175	Sequence 175, App
18	531.2	33.0	561	6	PCR-US95-01185-175	Sequence 175, App
19	529.4	32.8	555	3	US-08-693-182-1	Sequence 1, Appl
20	529.4	32.8	555	4	US-09-008-482-1	Sequence 1, Appl
21	526.2	32.6	555	4	US-08-945-529-1	Sequence 1, Appl
22	526.2	32.6	555	4	US-08-945-529-4	Sequence 4, Appl
23	526.2	32.6	555	4	US-08-945-529-5	Sequence 5, Appl
24	526.2	32.6	555	4	US-08-945-529-6	Sequence 6, Appl
25	525	32.6	525	1	US-08-009-973-2	Sequence 2, Appl
26	491	30.5	555	4	US-08-945-529-7	Sequence 7, Appl

; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; APPLICATION NUMBER: 449,447
; FILING DATE: 12-DEC-1989
; APPLICATION NUMBER: 860,883
; FILING DATE: 08-MAY-1986
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; SEQ ID NO: 1:
; LENGTH: 1145
; 5510472-1

Query Match 35.0%; Score 563.6; DB:7; Length 1145;
Best Local Similarity 99.3%; Pred. No. 2.9e-136;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1042 ccagtcacccagagagattccaaagatgtagcgcgccacacagacagcactcacc 1101
DB 171 ccagtcacccagagagattccaaagatgtagcgcgccacacagacagcactcacc 230
QY 1102 tcttcagaacgaattgacaaacaaattcgtgtacatctctgcagcggcatctcagccctgaga 1161
DB 231 tcttcagaacgaattgacaaacaaattcgtgtacatctctgcagcggcatctcagccctgaga 290
QY 1162 aaggagacatgtacaagaagtaacatgtgtgaagaagcagcaagagcactggcagaaaaac 1221
DB 291 aaggagacatgtacaagaagtaacatgtgtgaagaagcagcaagagcactggcagaaaaac 350
QY 1222 aacctgaacctccaaagatgctgaaagaagatggtgttccaatctcgtgattcaatgag 1281
DB 351 aacctgaacctccaaagatgctgaaagaagatggtgttccaatctcgtgattcaatgag 410
QY 1282 gagacttgctggtgaaatcatcactggtgttttggagttgaggtatcacctagagtac 1341
DB 411 gagacttgctggtgaaatcatcactggtgttttggagttgaggtatcacctagagtac 470
QY 1342 ctccagaacagattgagagtagtgaggaaacagcagagcagcgtgtgcagatgagtagacaaa 1401
DB 471 ctccagaacagattgagagtagtgaggaaacagcagagcagcgtgtgcagatgagtagacaaa 530
QY 1402 gtccgtgacagttctcgcagaaaaagcagaaagatctagatgcaataaccacctgac 1461
DB 531 gtccgtgacagttctcgcagaaaaagcagaaagatctagatgcaataaccacctgac 590
QY 1462 ccaaccacaaatgccagcctgctgcagagctgcagagctgcaggcacagaaaccagtggtgcaggac 1521
DB 591 ccaaccacaaatgccagcctgctgcagagctgcagagctgcaggcacagaaaccagtggtgcaggac 650
QY 1522 atgacaactcatctcattctgcagcgtttaaaggagttcctgcagtcagcctgagggct 1581
DB 651 atgacaactcatctcattctgcagcgtttaaaggagttcctgcagtcagcctgagggct 710
QY 1582 ctccgcaaatgacatgggcacccctga 1611
DB 711 ctccgcaaatgacatgggcacccctga 740

RESULT 7
US-08-437-680A-1
; Sequence 1, Application US/08437680A
; Patent No. 5681723
; GENERAL INFORMATION:
; APPLICANT: Ciliberto, Gennaro
; APPLICANT: Savino, Rocco
; TITLE OF INVENTION: Mutant Interleukin 6 with Improved
; TITLE OF INVENTION: Biological Activity Over Wild Interleukin 6
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: P.O. Box 747

; CITY: Falls Church
; STATE: VA
; COUNTRY: US
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,680A
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1264-133P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 base pair
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Adult
; CELL TYPE: monocyte
; IMMEDIATE SOURCE:
; LIBRARY: CDNA
; CLONE: pB.B2.21
; US-08-437-680A-1

Query Match 34.2%; Score 551.8; DB 1; Length 555;
Best Local Similarity 99.6%; Pred. No. 2.5e-133;
Matches 553; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1042 ccagtcacccagagagattccaaagatgtagcgcgccacacagacagcactcacc 1101
DB 1 CCAGTACCCCCAGGAGAGATTCCAAAGATGTAGCGCCCCACACAGACAGCCACTCACC 60
QY 1102 tcttcagaacgaattgacaaacaaattcgtgtacatctcgcagcggcatctcagccctgaga 1161
DB 61 TCTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCGACGGCATCTCAGCCCTGAGA 120
QY 1162 aaggagacatgtacaagaagtaacatgtgtgaagaagcagcaagagcactggcagaaaaac 1221
DB 121 AAGGAGACATGTAAACAAGAGTAACATGTGTGAAAGCAGCAAGAGAGGCACTGGCAGAAAAAC 180
QY 1222 aacctgaacctccaaagatggtgaaagaagatggtgttccaatctcgtgattcaatgag 1281
DB 181 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGTATCTCCAATCTCGATTCAATGAG 240
QY 1282 gagacttgctggtgaaatcatcactggtgttttggagttgaggtatcacctagagtac 1341
DB 241 GAGACTTGCTGTTGAAATCATCACTGCTCTTTTGGAGTTTGAGGTATACCTTAGGTAGTAC 300
QY 1342 ctccagaacagattgagagtagtgaggaaacagcagagcagcgtgtgcagatgagtagacaaa 1401
DB 301 CTCACAGAACAGATTTGAGAGTAGTGAGGAGAACAAAGCAGAGCTGTCCAGATGAGTACAAAA 360
QY 1402 gtccgtgacagttcctcgcagaaaaagcagaaagatctagatgcaataaccacctgac 1461
DB 361 GTCCTGATCCAGTTCTCTGCAAAAAAGGAGAAATCTAGATGCAATAAACACCCCTGAC 420
QY 1462 ccaaccacaaatgccagcctgctgcagagcgtgcagagcagacagaaaccagtggtgcaggac 1521

Db 421 CCACCCACCAATGCCAGCTGCTGACGAAGCTGCAAGGCACAGACCACTGGCTCAGGAC 480

QY 1522 atgacaactcatctattcgcgcagctttaaaggaggttcctgcagtcacagcctgagggct 1581

Db 481 ATGACACTCATCTCATTCCTGGGAGCTTAAAGGAGTTCCTGCAGTCCAGCCTGAGGCT 540

QY 1582 cttcggcaaatgtag 1596

Db 541 CTTTCGGCAAAATGTAG 555

```

RESULT      8
US-07-745-382-19
; Sequence 19, Application US/07745382
; Patent No. 5270181
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: LaVallie, Edward
; TITLE OF INVENTION: Peptide and Protein Fusions To
; TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules

```

CONFIDENTIAL REPORT.

ADDRESS: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

```

, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/07/745,382
, FILING DATE: 19910814
, CLASSIFICATION: 435
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/652,531
, FILING DATE: 06-FEB-1991
, ATTORNEY/AGENT INFORMATION:

```

```

, , REFERENCE/DOCKET NUMBER: G15188A
, ,
, , TELECOMMUNICATION INFORMATION:
, ,
, , TELEPHONE: (617) 876-1170
, ,
, , TELEFAX: (617) 876-5851
, ,
, , INFORMATION FOR SEQ ID NO: 19:
, ,
, , SEQUENCE CHARACTERISTICS:
, ,
, , LENGTH: 561 base pairs
, ,
, , TYPE: NUCLEIC ACID
, ,
, , STRANDEDNESS: double
, ,
, , TOPOLOGY: unknown
, ,
, , MOLECULE TYPE: DNA (genomic)
, ,
, , FEATURE:
, ,
, , NAME/KEY: CDS
, ,
, , LOCATION: 1..558
, ,
, , US-07-745-382-19

```

Query Match 34.1%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0;

1097	tcacctcttcagaaacgaattgacaaacaaattcggtagatctctcgagcggtcatctcagccc	1156	
Qy			
Ddb	2	TGGCTCCAGTACCTCCAGGTGAAGATTCTAAAGATGTAGCGGCCCCACACAGACGCCAC	61
Ddb	62	TCACTCTTTAGACGAGAAATTCACAAAACAAATTCGGTATCATCTCTCGACGGCATTTCAGCCC	121

Qy	1157	tgagaaggagacatgtaacaagagtaacatgtgtgaagcagcaaaagagcactggcag	12116
Db	122	TGAGAAAGGAGACATGTAACAAGAGTAACATGTGTGAAGCAGCAAAAGAGCACTGGCAG	181
Qy	1217	aaacaacctgaaccttccaaagatggctgaaaaagatggatgcttccaatctggattca	12716
Db	182	AAACAACCTTGAACCTTCCAAAGATGGCTTGA AAAAGATGGATGCTTCCAACTTCGGATTCA	241
Qy	1277	atgaggagacttgcctgggtgaaaaatcatcactggctcttttggagtttggaggtatacactag	13316
Db	242	ATGAGGAGACTTGCCTTGGTGAAAATCATCACCTGGCTCTTTTGGAGTTTGAGGTATACCTAG	301
Qy	1337	agtaacctccagaacagatttgagagtagtgagaaacaagccagagctgtgcagatgagta	13916
Db	302	AGTACTCCAGAACAGATTTGAGAGTAGTGAAGAAACAAGCCAGACAGCTGTGCAGATGAGTA	361
Qy	1397	caaaagtctctgattccagttccttcgacaaaaggcaaaagaatctagatgcataaccaccc	14516
Db	362	CAAAAGTCTGATCCAGTTCTCTCGACAAAAGGCAAAAGAACTAGATGCAATATACCACC	421
Qy	1457	ctgacccaacacaaatgcaagcctgtctgaagaaagctcagggcacagaacagtggtctgc	15116
Db	422	CTGACCCCAACCAAAATGCGACCGCTGCTGACGAAGCTCGAGGCACAGAACCCAGTGGCTGC	481
Qy	1517	aggacatgacaactcatctcattctgcgcagctttaaggagttcctcagttccagcctga	15716
Db	482	AGACATGACACTCATCTCATCTTCTGGCAGCTTTAAGAGTTCTCTGCAGTCCAGCCTGA	541
Qy	1577	gggctcttcggcaaatgtag	15916
Db	542	GGGCTCTTCGGCAAAATGTAG	561

```

RESULT          9
US-07-921-848-19
; Sequence 19, Application US/07921848
; Patent No. 5292646
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: LaVallie, Edward
; TITLE OF INVENTION: Peptide and Protein Fusions To
; TITLE OF INVENTION: Thioresoxin and Thioresoxin-Like Molecules
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/921,848
; FILING DATE: 19920728
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/652,531
; FILING DATE: 06-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,382
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI5188A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:

```


SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-07-921-848-19

Query Match 34.1%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1037 tcagcagctaccccccaggaagattccaaagatgtagcgcgcacacagacagccac 1096
Db 2 TGGCTCCAGTACCTCCAGGTGAAGATTCTAAAGATGTAGCGCGCCACACAGACGCCAC 61
QY 1097 tcacctcttcagacgaattgacaaacaaattcggtacatctctcgacgcatctcagccc 1156
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTCGGTACATCTCGAGCGGATCTCAGCCC 121
QY 1157 tgaaaggagacatgtacaagatgacatgtgtgaaagcagcaaaagagcactgacag 1216
Db 122 TGAGAAAGGAGACATGTAAACAGATGAACATGTGTGAAGCAGCAAAAGAGCGACTGGCAG 181
QY 1217 aaaaacacctgaacctccaaagatggctgaaagagatggatgcttccatctggattca 1276
Db 182 AAAACAACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCA 241
QY 1277 atgagagacttcctgggtgaaatacatcactgtcttttggagtttgaggtataacctag 1336
Db 242 ATGAGGAGACTTCGCTGGTGAATAATCATCTACTGCTCTTTTGGAGTTTGAGGTATACCTAG 301
QY 1337 agtacctccagaacagatttgagagtagtgaggaaacagcagagctgtgcagatgagta 1396
Db 302 AGTACCTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA 361
QY 1397 caaagctctgtatccagttctcagaaaggaagcaagaatctagatgcaataaccaccc 1456
Db 362 CAAAAGTCTGTATCCAGTTCTCTCAGAAAAAGGCAAGAATCTAGATGCAATAACCCACCC 421
QY 1457 ctgaccaaccacaaatgccagctctgacgaagctgacgacacagcaaacagctgctgc 1516
Db 422 CTGACCAACCAACAAATGCCAGCTCTGACGAAGCTGCGAGGCACAGAACCAAGTGGCTGC 481
QY 1517 aggacatgacaactcatctctcattctgcgcagctttaaggagttcctgagctccagcctga 1576
Db 482 AGGACATGACAACCTCATCTCATCTGCGCAGCTTTAAGGAGTTTCTGCAGTCCAGCCTGA 541
QY 1577 gggctcttcggcaaatgtag 1596
Db 542 GGGCTCTTCGGCAATGTAG 561

RESULT 10
US-08-165-301A-19
Sequence 19, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Dblasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: LaVallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
THIOREDOXIN-LIKE MOLECULES
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meiner, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..558
US-08-165-301A-19

Query Match 34.1%; Score 550.4; DB 1; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1037 tcagcagctaccccccaggaagattccaaagatgtagcgcgcacacagacagccac 1096
Db 2 TGGCTCCAGTACCTCCAGGTGAAGATTCTAAAGATGTAGCGCGCCACACAGACGCCAC 61
QY 1097 tcacctcttcagacgaattgacaaacaaattcggtacatctctcgacgcatctcagccc 1156
Db 62 TCACCTCTTCAGAACGAATTGACAAACAATTCGGTACATCTCTCGAGCGGATCTCAGCCC 121
QY 1157 tgaaaggagacatgtacaagatgacatgtgtgaaagcagcaaaagagcactgacag 1216
Db 122 TGAGAAAGGAGACATGTAAACAGATGAACATGTGTGAAGCAGCAAAAGAGCGACTGGCAG 181
QY 1217 aaaaacacctgaacctccaaagatggctgaaagagatggatgcttccatctggattca 1276
Db 182 AAAACAACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCA 241
QY 1277 atgagagacttcctgggtgaaatacatcactgtcttttggagtttgaggtataacctag 1336
Db 242 ATGAGGAGACTTCGCTGGTGAATAATCATCTACTGCTCTTTTGGAGTTTGAGGTATACCTAG 301
QY 1337 agtacctccagaacagatttgagagtagtgaggaaacagcagagctgtgcagatgagta 1396
Db 302 AGTACCTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA 361
QY 1397 caaagctctgtatccagttctcagaaaggaagcaagaatctagatgcaataaccaccc 1456
Db 362 CAAAAGTCTGTATCCAGTTCTCTCAGAAAAAGGCAAGAATCTAGATGCAATAACCCACCC 421
QY 1457 ctgaccaaccacaaatgccagctctgacgaagctgacgacacagcaaacagctgctgc 1516
Db 422 CTGACCAACCAACAAATGCCAGCTCTGACGAAGCTGCGAGGCACAGAACCAAGTGGCTGC 481
QY 1517 aggacatgacaactcatctctcattctgcgcagctttaaggagtttccagctccagcctga 1576
Db 482 AGGACATGACAACCTCATCTCATCTGCGCAGCTTTAAGGAGTTTCTGCAGTCCAGCCTGA 541

QY 1577 gggctcttcggcaaatgtag 1596
|||||
Db 542 GGGCTCTCGGCAATGTAG 561

RESULT 11

PCT-US94-14179-19
; Sequence 19, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinert, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..558
PCT-US94-14179-19

Query Match 34.1%; Score 550.4; DB 6; Length 561;
Best Local Similarity 98.9%; Pred. No. 5.7e-133;
Matches 554; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1037 tcgagccgtaccgccaggaagattccaaagatgtagccgccccacacagacagccac 1096
|||||
Db 2 TGGCTCCAGTACCTCCAGGTGAAGATTCTAAGATGTAGCCGCCCCACACAGACAGCCAC 61
QY 1097 teacctcttcagaagaattgacaacaaattcgtacatctctgcagcgcatctcagccc 1156
|||||
Db 62 TCACCTCTTCAGAACGAATTGACAAACAAATTCGTACATCTCGACGGCATCTCAGCCC 121
QY 1157 tgagaaaggagacatgtacaagagtaicacatgtgtgaagcagcaaaaggagcactggcag 1216
|||||
Db 122 TGAGAAAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAAAGGAGCACTGGCAG 181
QY 1217 aaaaacactgaacctccaaagatggctgaaaagatggatgttccaatctggattca 1276
|||||
Db 182 AAACAACTGAACCTTCCAAAGATGGCTGAAAGAGATGGATGCTTCCAACTTGGAATCA 241

QY 1277 atgaggagacttgctgggtgaaaaatcatcactggtctcttttgaggttgaggtatacctag 1336
|||||
Db 242 ATGAGGAGACTTGGCTGGTGAAAAATCATCATTCTGGTCTTTTGGAGTTGAGGTATACCTAG 301
QY 1337 agtacctccagaacagatttgagtagtgaggaagaagccagagctgtgcagatgagta 1396
|||||
Db 302 AGTACTCCAGAACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTA 361
QY 1397 caaaagtctgatccagttctctgcagaaaaagcaaaagaaatctagatgcaataaacaccc 1456
|||||
Db 362 CAAAAGTCTGTATCCAGTTCCTGCAGAAAAAGGCAAAATCTAGATGCCAATAAACACCC 421
QY 1457 ctgaccccaaccacaatgccagctgctgacgaagctgcagacacagacagtagtgctgc 1516
|||||
Db 422 CTGACCCCAACCAAAATGCCAGCCCTGCTGACGAAGCTGCAGGCACAGAACCAAGTGGCTGC 481
QY 1517 aggcacatgacaaactcatctctgcgcagctttaaagagttcctgcagtcagcctcga 1576
|||||
Db 482 AGGCATGACAACTCATCTCAATTCGCGCAGCTTTAAGGAGTTCTCGAGTCCAGCCTGA 541
QY 1577 gggctcttcggcaaatgtag 1596
|||||
Db 542 GGGCTCTTCGGCAATGTAG 561

RESULT 12

US-08-469-318-57
; Sequence 57, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-318-57

Query Match 33.4%; Score 538.6; DB 5; Length 951;
Best Local Similarity 95.0%; Pred. No. 7.6e-130;
Matches 556; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1009 ggtggaggttcttgaggtggaggttctctgcagccagtcaccgccagagagagattccaaa 1068
|||||
Db 367 GGTGGTGTCTTGGGGGGGCTCCAAACATGGCTCCAGTACCACAGGTGAGATTCCAAA 426
QY 1069 gatgtagccgccccacacagacagccactcctcttcagacgaattgacaaacaaatt 1128
|||||
Db 427 GATGTGGCGGCCCCACACAGACAGCCACTCCTCTTCAGAACGAATTCACAAACAAT 486
QY 1129 cgtgtacatcttcgacgcacatctcagcctgagaagagacatgatacaagagtaacatg 1188
|||||
Db 487 CGGTACATCTTCGACGGGATATAGCCTTGAAAGAGAGACATGTAAACAGAGTAACATG 546
QY 1189 tgtgaagcagcaaaaggagcactggcagaaaaaacctgaaccttccaaagatggctgaa 1248

Db 547 TGTGAAGCAGCAAGAGCGCTAGCAGAAAACAACCTGAACCTTCCAAAGATGGCTGAA 606
QY 1249 aaagatggatgttccaatctgattcaatgagagacttgcctggtgaaataatcatcact 1308
Db 607 AAAGATGGATGCTTCCAATCCGATTCATGAGGAGACTTGCCTGTGTGAAAATCATCACT 666
QY 1309 ggtctttggagtttgaggtatatacttagagtagtaccctccagacaagatttgagagtagtgag 1368
Db 667 GGTCTTTGGAGTTTGAGGTATACCTCGAGTACTCCAGAACAGATTTGAGAGTAGTGAG 726
QY 1369 gaacaagccagagctgtgcagtagtgcagaaagtccctgagtagtccctgcagaaaaag 1428
Db 727 GAACAAGCCAGAGCTGTGCAGATGTGCACAAAAGTCTGTATCCAGTTCCTGTCAGAAAAAG 786
QY 1429 gcaagaatactagatgaataaaccacccctgaccccaacacaaatgccagcctgtgcag 1488
Db 787 GCAAGAATCTAGATGCAATTAACACCCCTGACCCCAACCAATGCATCCCTGCTGAGC 846
QY 1489 aagctgcagcagacagaccagtggtgcagagacatgacaaactcatctcattctgcgcagc 1548
Db 847 AAGCTGCAGCCACAGAACCAAGTGGTGCAGAGACATGACAACTCATCTCATCTTCTGCGCAGC 906
QY 1549 tttaaggagttcctgcagtcagcctgcagcctgcagcctgcagcctgcagcctgcagc 1593
Db 907 TTTAAGGAGTCTCGAGTCCAGCTGAGGGCTCTTCGGCAAAATG 951

RESULT 13
PCT-US95-01185-57
; Sequence 57, Application PC/TUS9501185
; GENERAL INFORMATION:
; APPLICANT: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01185
; FILING DATE: 02-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192325
; FILING DATE: 14-FEB-1994
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-01185-57

Query Match 33.4%; Score 538.6; DB 6; Length 951;
Best Local Similarity 95.0%; Pred. No. 7.6e-130;
Matches 556; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1009 ggtggaggttctgaggtggaggttctgtcgagccagtagcccccaggagagattccaaa 1068
Db 367 GGTGGTGGTGTCTGGCGCGCTCCACATGCTCCAGTACACACAGGTGAAGATTCCAAA 426
QY 1069 gatgtagcccccacacagacagccactcacctcttcagaacgaattgacaacaaatt 1128
Db 427 GATGTGCCGCCGCCACACAGACGCCACTCACCTCTTCAGAACGAATTGACAAACAAAT 486
QY 1129 cggtagatcctgcagcgcattctcagcctgcagaaagagagcatgtaacaagtagtaacatg 1188
Db 487 CGGTACATCTCGACGGGATATCAGCCCTCAGAAAGGAGACATGTAACAGAGTAAATG 546

QY 1189 tgtgaagcagcaaaagggcactggcagaaaaaacacctgaaccttccaaagatggctgaa 1248
Db 547 TGTGAAGCAGCAAGAGCGCTAGCAGAAAACAACCTGAACCTTCCAAAGATGGCTGAA 606
QY 1249 aaagatggatgttccaatctgattcaatgagagacttgcctggtgaaataatcatcact 1308
Db 607 AAAGATGGATGCTTCCAATCCGATTCATGAGGAGACTTGCCTGTGTGAAAATCATCACT 666
QY 1309 ggtctttggagtttgaggtatatacttagagtagtaccctccagacaagatttgagagtagtgag 1368
Db 667 GGTCTTTGGAGTTTGAGGTATACCTCGAGTACTCCAGAACAGATTTGAGAGTAGTGAG 726
QY 1369 gaacaagccagagctgtgcagtagtgcagaaagtccctgagtagtccctgcagaaaaag 1428
Db 727 GAACAAGCCAGAGCTGTGCAGATGTGCACAAAAGTCTGTATCCAGTTCCTGTCAGAAAAAG 786
QY 1429 gcaagaatactagatgaataaaccacccctgaccccaacacaaatgccagcctgtgcag 1488
Db 787 GCAAGAATCTAGATGCAATTAACACCCCTGACCCCAACCAATGCATCCCTGCTGAGC 846
QY 1489 aagctgcagcagacagaccagtggtgcagagacatgacaaactcatctcattctgcgcagc 1548
Db 847 AAGCTGCAGCCACAGAACCAAGTGGTGCAGAGACATGACAACTCATCTCATCTTCTGCGCAGC 906
QY 1549 tttaaggagttcctgcagtcagcctgcagcctgcagcctgcagcctgcagcctgcagc 1593
Db 907 TTTAAGGAGTCTCGAGTCCAGCTGAGGGCTCTTCGGCAAAATG 951

RESULT 14
PCT-US94-12873-3
; Sequence 3, Application PC/TUS9412873
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 26
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44Mb, double side, high density
; OPERATING SYSTEM: MS-DOS Version 6
; SOFTWARE: WORD for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12873
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
PCT-US94-12873-3

Query Match 33.4%; Score 538.4; DB 6; Length 540;
Best Local Similarity 99.8%; Pred. No. 6.9e-130;
Matches 539; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1057 gaagattccaaagatgtagcgccccacagacagccactcacctcttcagaaacgaatt 1116
Db 1 GAAGATTCCAAAGATGTAGCGCGCCCCACACAGACAGAGCCACTCCTTTCAGAACGAAAT 60
QY 1117 gacaaacaaattcgggtacatctctgcagcgcatctcagccctgagaaaggagacatgtaac 1176
Db 61 GACAAACAAATTCGGTACATCTCTCGAGCGCATCTCAGCCCTGAGAAAGGAGACATGTAAC 120
QY 1177 aagatgaacatgtagtgaagcagcaagagagcactgagcaaaaaaacacctgaacctcca 1236
Db 121 AAGAGTAACATGTGTGAAGAGCAGCAAGAGGCACTGGCAGAAAAACAACCTGAACCTTCCA 180
QY 1237 aagatggtgaaaaagatgtagtcttccaatctgattcaatgagagacttgcctggtg 1296

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2000, 09:34:22 ; Search time 80.09 Seconds
(without alignments)
5035.705 Million cell updates/sec.

Title: US-09-142-471-3

Perfect score: 1612
Sequence: 1 gtcacgcagtgagtgtag.....gtacgatggccacgctcgac 1612

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1587	98.4	1627	1 T97848	Human fusion polyp
2	1482	91.9	1552	1 T97849	Human fusion polyp
3	995	61.7	2061	1 N90340	Sequence encoding
4	995	61.7	2066	1 Q41746	IL-6 receptor codi
5	995	61.7	2087	1 N90847	DNA contg. region
6	995	61.7	3319	1 V60295	Human interleukin-
7	993.4	61.6	1486	1 V60296	Human interleukin-
8	993.4	61.6	3319	1 T31441	Interleukin-6 rece
9	969	60.1	1074	1 V04440	Interleukin 6 rece
10	565.2	35.1	1139	1 N90255	Interleukin-6. New
11	565.2	35.1	1139	1 N80259	Interleukin 6. Pro
12	585.2	35.1	1162	1 Q01763	BSF-2 gene for hum
13	583.6	35.0	1101	1 N90131	DNA sequence of pB
14	563.6	35.0	1101	1 N90135	DNA sequence of pB
15	563.6	35.0	1101	1 N90345	Plasmid pBSF2-L8,
16	563.6	35.0	1128	1 Q74057	Human interleukin
17	563.6	35.0	1128	1 V60294	Human interleukin-
18	563.6	35.0	1145	1 N90377	Interferon-beta-2
19	563.6	35.0	1145	1 N70348	Sequence of human
20	563.6	35.0	1145	1 Q39582	IFN-beta-2a coding
21	563.6	35.0	1145	1 Q86523	cDNA encoding inte
22	563.6	35.0	1161	1 N81460	Sequence encoding
23	562	34.9	1101	1 N80966	Plasmid pBSF2-L8.
24	562	34.9	1101	1 N81517	Sequence encoding
25	558.8	34.7	1099	1 Q25831	Mutant human BCFP.
26	558	34.6	1165	1 Q56265	Sequence of human
27	555	34.4	639	1 N91706	Human interleukin-
28	554	34.4	1162	1 Q11824	B cell differentia
29	552.2	34.3	566	1 N80300	Interleukin 6. Pro
30	551.8	34.2	555	1 Q65465	Mutant Interleukin
31	550.4	34.1	561	1 Q56903	Human Interleukin
32	550.4	34.1	561	1 Q90773	Human Interleukin-
33	549	34.1	560	1 Q03365	Segment of human B

34	547.2	33.9	555	1 Q00977	Segment of human B
35	547.2	33.9	561	1 Q27479	Encodes human IL-6
36	547.2	33.9	636	1 Q55973	Human interleukin-
37	545.6	33.8	555	1 Q02027	Gene segment of B-
38	539.2	33.4	586	1 N91644	Synthetic interleuk
39	538.4	33.4	540	1 Q87153	Human interleukin-
40	536.2	33.3	663	1 T64947	Human interleukin-
41	534.2	33.1	555	1 T32818	Interleukin-6 codi
42	526.6	32.7	695	1 T64948	Human interleukin
43	526.2	32.6	555	1 T44357	cDNA encoding huma
44	526.2	32.6	555	1 T44356	Human interleukin
45	526.2	32.6	555	1 T44358	cDNA encoding huma

ALIGNMENTS

RESULT 1

ID	T97848	standard; DNA; 1627 BP.
AC	T97848;	
DT	25-MAR-1998	(first entry)
DE	Human fusion polypeptide H-IL-6 DNA containing a 18 amino acid linker.	
KW	Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;	
KW	protein interaction; therapeutic; antagonist; ss.	
OS	Synthetic.	
OS	Homo sapiens	
FH	Key	Location/Qualifiers
FT	CDS	34..1611
FT		/*tag= a
FT	sig_peptide	34..90
FT		/*tag= b
FT	mat_peptide	91..1608
FT		/*tag= c
FT		/product= H-IL-6
FT		/note= "fusion polypeptide"
PN	WO9732891-A2.	
PD	12-SEP-1997.	
PF	07-MAR-1997;	D00458.
PR	07-MAR-1996;	DE-008913.
PA	(ANGE-) ANGEWANDTE GENTECNOLOGIE SYSTEME GMBH.	
PI	Rose-John S;	
DR	WPI; 97-470535/43.	
DR	P-PSDB; W36846.	
PT	Conjugate of two peptide(s) with mutual affinity connected by a	
PT	linker - used to modulate interactions between proteins, e.g. for ex	
PT	vivo expansion of human stem cells	
PS	Claim 12; Fig 1; 19pp; German.	
CC	This sequence encodes the fusion polypeptide H-IL-6 which contains an	
CC	18 amino acid linker which joins the carboxy terminus of human	
CC	interleukin-6 receptor (IL-6R) with the amino terminus of human	
CC	interleukin-6 (IL-6). Such conjugates could be used to modulate	
CC	interactions between proteins, particularly to overcome interrupted	
CC	interactions caused by an incomplete interleukin-6 (IL-6) receptor. These	
CC	constructs derived from IL-6 and its receptor, can also be used for ex	
CC	vivo expansion of human stem cells, and as a therapeutic IL-6 receptor	
CC	antagonist.	
SQ	Sequence 1627 BP; 388 A; 450 C; 481 G; 308 T;	

Query Match	98.4%;	Score 1587;	DB 1;	Length 1627;
Best Local Similarity	99.1%;	Pred. No. 0;		
Matches 1612;	Conservative 0;	Mismatches 0;	Indels 15;	Gaps 1;
Qy	1	gtcagcagcatgagtggttagccgagaggaagcatgctggtcggtcggtcggtcggtcggtg 60		
Db	1	gtcagcagcatgagtggttagccgagaggaagcatgctggtcggtcggtcggtcggtcggtg 60		
Qy	61	gctgcctctgctggtcggtcggtcggtcggtcggtcggtcggtcggtcggtcggtcggtg 120		
Db	61	gctgcctctgctggtcggtcggtcggtcggtcggtcggtcggtcggtcggtcggtcggtg 120		
Qy	121	gtggcaagagcgctgctgacctgctgccaggagacagcgctgactgacctgacctgccccg 180		

QY	1021	ggaggtggaggttctgtcgagccaggtacccccaggaggaagtcccaagatgtaccgcc	1080
DB	961	GGAGGTGGAGGTTCTGTGCGAGCCAGTACCCCCAGGAGAAGATTCCAAAGATGTAGCCGCC	1020
QY	1081	ccacagacagccactcaacctcttcagaacgaattgacaaacaattcgggtacatctc	1140
DB	1021	CCACACAGACAGCCACTCCTCTTCCAGAACGAATTTGACAAACAATTCGGTACATCTCTC	1080
QY	1141	gacggcatctcagccctgagaaagagagacatgttaacaagagttaacatgtgtgaaagcagc	1200
DB	1081	GACGGCATCTCAGCCCTGAGAAAGGAGACATGTACACAGAGTAAATGTGTGAAAGCAGC	1140
QY	1201	aaagaggcaatgvcagaaaaaacacctgaaccttccaaagatggctgaaagaatggtatgc	1260
DB	1141	AAAGAGGCACCTGGCAGAAAAACAACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGC	1200
QY	1261	ttcaactctgattcaatgaggagaccttgccctgggtgaaaaatcatcaactggctcttttgag	1320
DB	1201	TTCCAATCTGGATTCAATGAGGAGACTTGCCCTGGTGAATAATCATCACCTGGCTCTTTTGAG	1260
QY	1321	tttgaggtatccttagtagtacctccagaaacagattgttgagtagtgaggaagaacagccaga	1380
DB	1261	TTTGAGGTATACCTAGAGTACCTCCAGAACAGATTGAGAGTAGTGAGNACAAGCCAGA	1320
QY	1381	gctgtcagatgagtacaaagtctcgtatccagttctctcagaaaaagcgaagaatcta	1440
DB	1321	GCTGTGCAGATGAGTACAAAAGTCTGTAGTCCAGTTCTCAGAAAAAGCAAGAATCTA	1380
QY	1441	gatcaataaccaccctcgaccacacacaaatgccagctcgtgacgaagctgcaggca	1500
DB	1381	GATCAATAACACCCCTGACCCCAACCAATGCGCAGCTCCTCAGCAAGCTGCAGGCA	1440
QY	1501	cagacacagtggtctgcaggacatgacaactcatctctatctcgcagctttaagaggttc	1560
DB	1441	CAGAACCAAGTGGCTGCAGGACATGACACATCATCTCTTCGCGACGCTTTAAGAGGTTT	1500
QY	1561	ctgcagtcacgctgagggtctctcggcaaatgtagcatggcgacccgtcgac	1612
DB	1501	CTGCAGTCCAGCCTGAGGGCTCTTCGGCAAAATGTAGCATGGGACCGTCGAC	1552
RESULT	3		
ID	N90340	ID N90340 standard; cDNA; 2061 BP.	
AC	N90340;		
DT	31-MAR-1992 (first entry)		
DE	Sequence encoding a receptor protein for human B cell stimulating factor-2 (BSF2 receptor).		
KW	B cell; immune disorder;		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	cds	247..1753	
FT		/*tag= a	
FT		/note= "SQ claimed"	
PN	EP-325474-A.		
PD	26-JUL-1989.		
PF	20-JAN-1989; 300536.		
PR	22-JAN-1988; JP-012387.		
PR	25-JAN-1988; JP-012599.		
PR	04-AUG-1988; JP-194885.		
PR	14-JAN-1989; JP-017461.		
PR	20-JAN-1989; JP-009774.		
PA	(KISH/) KISHIMOTO T.		
PI	Kishimoto T;		
DR	WPI; 89-214667/30.		
DR	P-PSDB; P90284.		
PT	Receptor protein for human B cell stimulating factor-2 - obt'd. by recombinant DNA techniques and used as diagnostic, prophylactic or therapeutic agent		
PS	Disclosure; Fig 3; 63pp; English.		
CC	The cDNA in N90340 was derived from monocyte cell line U937.		
CC	Isolated BSF2 receptor and DNA encoding it are claimed, as are		
CC	(c) expression vectors; (c) host organisms; (d) antibodies; and		

Db	926	TTCTGTCCCGAGGAGATTGGCGAAGCGGAGTGGACCGGAGCCCATGG	985
Qy	968	gcacgccttgacagaatccaggagtcctccagct	1002
Db	986	GCAGCCCTTGGACAGATCCAGGAGTCTCCAGCT	1020
RESULT	8		
T31441			
ID	T31441	standard; cDNA; 3319 BP.	
AC	T31441		
DT	28-NOV-1996	(first entry)	
DE	Interleukin-6 receptor coding sequence.		
KW	Interleukin-6; IL; receptor; antisense oligonucleotide; inhibition;		
KW	gene expression; kidney tumour; myeloma; Kaposi's sarcoma; psoriasis;		
KW	rheumatoid arthritis; endotox shock; ss.		
OS	Homo sapiens.		
PH	Key	Location/Qualifiers	
FT	CDS	438..1844	
FT		/*tag= a	
FT		/product= Interleukin-6 receptor.	
PN	W09618416-A1.		
PD	20-JUN-1996.		
PF	15-DEC-1995; J02587.		
PR	16-DEC-1994; JP-313167.		
PR	18-AUG-1995; JP-210739.		
PI	(CHUS) CHUGAI SEIYAKU KK.		
PI	Koishibara Y, Kuromaru K;		
DR	WPI; 96-300392/30.		
DR	P-PSDB; R98364.		
PT	Anti-sense oligo:nucleotide inhibitor against human IL-6R expression		
PT	- for treatment of e.g. tumours, cancers, rheumatoid arthritis,		
PT	psoriasis, endo:toxic shock, etc.		
PS	Claim 2; Page 17-21: 32pp; Japanese.		
CC	Antisense oligonucleotides may be used to inhibit the expression of		
CC	the interleukin-6 receptor. Inhibition of expression of the		
CC	IL-6 receptor is useful in the treatment of kidney tumours, myeloma,		
CC	Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotox		
CC	shock. The antisense oligonucleotides are administered at a dosage		
CC	of 0.1-100mg/kg, pref. 0.1-50 mg/kg.		
CC	Sequence 3319 BP; 735 A; 937 C; 960 G; 687 T;		
Qy	8	catgagtggttagccgaggaggagatgtgcccgtgcgtgcgcgtgcgtgcgtgcgc	67
Db	412	CATGAGTGTGTGAGCGAGGAGGAGCATGTGCGCGTGCCTGCGCGCTGCTGGCTGCC	471
Qy	68	tgcctggccgcgcggagcgcctgcccccaagcgcctccctgcgcagagtgcaa	127
Db	472	TGCTGTGCCCGCCCGGAGCGCGCTGCCCCCAAGCGCTGCCCTTCGCGAGAGTGCCAA	531
Qy	128	gaggcgtgctgaccagtgctgcaggagagacgctgacctgacctgcgcgggggtagagc	187
Db	532	GAGGCGTGTGACCACTGTGCGCAGGAGACACGCTGACTCTGACCTGCGCGGGGTAGAGC	597
Qy	188	cggaagacaatgcacactgttcaactgggtgctcaggaagcggctgcaggctccacccca	247
Db	592	CGGAAGACAATGCCACTGTTTCACTTGGTGTCTCAGAAAGCGGCTGACAGGTCCACCCCA	651
Qy	248	gcagatggcctggcatgggaagagcgtgctgctgaagtcggtgcagctccagactctg	307
Db	652	GCAGATGGGCTGGCATGGGAAGGAGGTGCTTGTCTGTGAGTGGTGGTGCAGCTCCACGACTGT	711
Qy	308	gaactatctcatgctacccggccggcccgactggtggactgtgacctgtgctggtggtg	367
Db	712	GAACATATTATGTCACCGGGCCGCCCGCAGCTGGGACTGTGCATCTTCTGGTGGATG	771
Qy	368	tccccccgagagcccccagctctctctgcttcccggaagccccctcagcaatgtgttt	427

QY 1342 ctccagaacagattgtagagtagtgaggaacaaagccagagctgtgcagatgagtacaaaa 1401
 |||||
 Db 435 CTCACAGACAGATTGAGAGTAGTGAGGAACAACGCCAGAGCTGTGCAGATGAGTACAAA 494
 |||||
 QY 1402 gtctgtatccagttctctgcagaaaggaagcaaatctagatgcaataaccaccctgac 1461
 |||||
 Db 495 FTCTGTATCCAGTTCTCTCAGAAAAGCAAGAATCTAGATGCAATAAACACCCCTGAC 554
 |||||
 QY 1462 caaaccaaaatgccagctctcaagaagctgcagacacagaacacagctgctcaggac 1521
 |||||
 Db 555 CGAACCAAAATGCCAGCTCTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 614
 |||||
 QY 1522 atgacaactcatctctctgcagctttaaaggagttccctgcagtcagcctgagggct 1581
 |||||
 Db 615 ATGACAATCATCTATCTCGCAGCTTTAAGGAGTTCCTGCAGTCCAGCTCAGGGCT 674
 |||||
 QY 1582 ctccgcaaatgtagcatggcgacccgtcga 1611
 |||||
 Db 675 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 704
 |||||

RESULT 12

ID Q01763 standard; DNA; 1162 BP.
 AC Q01763;
 DT 27-JUL-1990 (first entry)
 DE BSF-2 gene for human B-cell differentiation factor.
 KW BSF-2; dhfr; dihydrofolic acid reductase; differentiation.
 OS Homo sapiens.
 FH key Location/Qualifiers
 FT cds 73..708
 FT /*tag= a
 PN J02009388-A.
 PD 12-JAN-1990.
 PE 8-JUL-1988; 170142.
 PR 9-MAR-1988; JP-055270.
 PA (AJIN) Ajinomoto KK.
 DR WPI; 90-055348/08.
 DR P-PSDB; R05415.
 PT Physiologically active protein prepn..
 PT by transforming plasmid having gene coding physiologically
 PT active protein and gene of dihydrofolic acid reductase to hamster
 PT ovary etc.
 PS Example 3; Fig 6; 12pp; Japanese.
 CC Gene may be expressed by transforming a dhfr negative strain of CHO cells
 CC with an active BSF-2 gene and dhfr carrying vector. The BSF-2 gene is
 CC a B-cell differentiating factor.
 SQ Sequence 1162 BP; 359 A; 237 C; 264 G; 302 T;

Query Match 35.1%; Score 565.2; DB 1; Length 1162;
 Best Local Similarity 99.5%; Pred. No. 7.6e-136;
 Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1042 ccagatccccagagagaattccaaagatgtagccgccccacacagacagccactcacc 1101
 |||||
 Db 157 CCAGTAGCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACACAGACCCACTCACC 216
 |||||
 QY 1102 tcttcagaacgaattgacaaacaaattcggtagatctcctgcagggcatctcagccctgaga 1161
 |||||
 Db 217 TCTTCAGAACGAATTGACAAACAAATTCGGTATATCTCGACGGCATCTCAGCCCTCAGA 276
 |||||
 QY 1162 aaggagacatgaaacagagttaacatgtgtgaagcagcaaaaggcactggcgagaaaac 1221
 |||||
 Db 277 AAGGAGACATGTACAGAGTAACTGTGTGAAGCAGCAAAAGAGGCACATGGCAGAAAAC 336
 |||||
 QY 1222 aacctgaacctccaaagatggctgtgaaagagatggatgcttccaatctggattcaatgag 1281
 |||||
 Db 337 AACCTGAACCTTCCAAAGATGGGTGAAAGAGATGGATGCTTCCAATCTGGATTCAATGAG 396
 |||||
 QY 1282 gagaacttgctgtgaaataatcactcactggtcttttgaggtttaggtatatacctagatc 1341
 |||||

Db 397 GAGACTTGCCTGGTGAAAAATCATCACTGCTTTTGGAGTTAGGTATACCTAGAGTAC 456
 |||||
 QY 1342 ctccagaacagattgtagagtagtgaggaacaaagccagagctgtgcagatgagtacaaaa 1401
 |||||
 Db 457 CTCCAGAACAGATTGAGAGTAGTGAGGAACAACGCCAGAGCTGTGCAGATGAGTACAAA 516
 |||||
 QY 1402 gtctgtatccagttctctgcagaaaggaagcaaatctagatgcaataaccaccctgac 1461
 |||||
 Db 517 GTCTGTATCCAGTTCCTGCAGAAAAGCAAGAATCTAGATGCAATAAACACCCCTGAC 576
 |||||
 QY 1462 ccaaccacaaatgccagctctgcagcagctgcagcagcagacagacaccagtgctgcagac 1521
 |||||
 Db 577 CCAACCAAAATGCCAGCTCTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 636
 |||||
 QY 1522 atgacaactcatctctctgcagcagctttaaaggagttccctgcagtcagcctgagggct 1581
 |||||
 Db 637 ATGACAATCATCTATCTCGCAGCTTTAAGGAGTTCCTGCAGTCCAGCTCAGGGCT 696
 |||||
 QY 1582 ctccgcaaatgtagcatggcgacccgtcga 1611
 |||||
 Db 697 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 726
 |||||

RESULT 13

ID N90131 standard; DNA; 1101 BP.
 AC N90131;
 DT 1-NOV-1989 (first entry)
 DE DNA sequence of pBSF2-L8
 KW pBSF2-L8; pGEM4; cDNA; clone; Fc epsilon R-gene; IgE; allergy.
 FH key Location/Qualifiers
 FT misc_feature 1..6
 FT /*tag= a
 FT cds 7..642
 FT /*tag= b
 FT misc_feature 1097..1101
 FT /*tag= c
 PN EP-321842-A.
 PD 28-JUN-1989.
 PE 14-DEC-1988; 120878.
 PR 22-DEC-1987; EP-100814.
 PA (OSAU) Osaka University.
 PI Kishimoto T, Suehara M, Kikutani H, Barsumian EL, Schneider FJ;
 DR WPI; 89-186249/26.
 DR P-PSDB; P90047.
 PT Cloned gene for eukaryotic expression of Fc epsilon receptor
 PT - for use in treatment and prophylaxis of allergy, esp. asthma.
 PS Disclosure; fig 3; 24pp; English.
 CC pBSF2-L8 is prep'd. by digesting pBSF-2.38 with HindIII and BamHI
 CC to obtain a 1.2 kbp EcoRI-BamHI BSF-2 cDNA insert. This was digested
 CC with HinfI, end-filled, and digested with KpnI. A 100 bp
 CC KpnI-HinfI fragment contg. BSF-2 leader sequence was cloned into
 CC the multiple cloning site of KpnI-SmaI digested pGEM4, and one of the
 CC selected clones named as pBSF2-L8. It is used in prep'n. of pSFC
 CC epsilon R-1 (see N90132). The misc. feature a is a KpnI site, and
 CC c is a BamHI site. The encoded peptide sequence (see P90047) includes
 CC that of the BSF-2 signal sequence.
 SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 35.0%; Score 563.6; DB 1; Length 1101;
 Best Local Similarity 99.3%; Pred. No. 1.9e-135;
 Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1042 ccagatccccagagagaagattccaaagatgtagccgccccacacagacagccactcacc 1101
 |||||
 Db 91 CCAGTAGCCCCAGGAGAAGATTCCAAAGATGTAGCCGCCCCACACACAGACCCACTCACC 150
 |||||
 QY 1102 tcttcagaacgaattgacaaacaaattcggtagatctcctgcagggcatctcagccctgaga 1161
 |||||
 Db 151 TCTTCAGAACGAATTGACAAACAAATTCGGTATATCTCTGCAGGCATCTCAGCCCTCAGA 210
 |||||
 QY 1162 aaggagacatgtaacaagagtagtaactgtgtgaaagcagcaagaggcactggcagaaaac 1221
 |||||

```
Db 211 AAGGAGACATGTAAACAGTAGTAACATGTGTGAAGCAGCAAAAGAGGCACTGGCAGAAAAC 270
QY 1222 aacctgaacctccaaagatggtcgaataagatgtagcttccaatctggattcaatgag 1281
Db 271 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCAATGAG 330
QY 1282 gagacttgccgtggtgaataatcatcactggtctctttggagtttgaggtatatacctagatgac 1341
Db 331 GAGACTTGCCGTGGAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 390
QY 1342 ctccagaacagattgagagtagtgaggaacaagccagagctgtgcagatgagtagtaaaaa 1401
Db 391 CTCCAGAAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTAGTACAAA 450
QY 1402 gtcctgatccagttcctgcagaaaaagcgaagaatctagatgcataataacacccctgac 1461
Db 451 GTCCGTGATCCAGTTCTCTGCAGAAAAGCAAGAATCTAGATGCAATTAACCAACCCCTGAC 510
QY 1462 ccaaccacaaatgccagcctgctgcagagctgcaggcacagaacacagtggtgcaggac 1521
Db 511 CCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCACTGGCTGCAGGAC 570
QY 1522 atgacaactatctctatctgcgcagctttaaggaggtctctgcagctccagcctgagggct 1581
Db 571 ATGACAACATCATCTATTCTGGCAGCTTTAAGGAGTCTCTGCAGTTCAGCCTGAGGGCT 630
QY 1582 cttcggcaaatgtagcatgggcacccgtcga 1611
Db 631 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 660

RESULT 14
N90135
ID N90135 standard; DNA; 1101 BP.
AC N90135;
DE 1-NOV-1989 (first entry)
DE DNA sequence of pBSF2-L8
DE Fc epsilon receptor; cloned gene; IgE; pBSF2-L8; allergy; asthma; BSF-2.
FH Key Location/Qualifiers
FT misc_feature 2..5
FT cds /*tag= a
FT /*tag= b
FT /*tag= c
FT misc_feature 1097..1101
FT EP-321601-A.
PN 28-JUN-1989.
PD 22-DEC-1987; 119080.
PR 22-DEC-1987; EP-119080.
PA (OSAU) Osaka University
PI Kishimoto T, Suemura M, Kikutani H, Barsumian E;
DR WPI; 89-186101/26.
DR P-PSDB; P90371.
DR Cloned genes coding for soluble IgE receptor - comprising modified coding
PT sequence of Fc epsilon receptor gene.
PS Disclosure: fig. 3; 20pp; English.
CC Sequence of pBSF2-L8, which is used as a vector in prepn. of plasmid
CC pSfc epsilon R-1. It is prepd. by inserting BSF-2 cDNA insert (from
CC pBSF-2.38) into pGEM4. Misc. feature a is a KpnI site, and c is a BamHI
CC site. See also N90134, N90136 and P90371 for encoded peptide.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 35.0%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 1.9e-135;
Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1042 ccagtaccctccagagagattccaaagatgtagcgcgcacacagacagaccactacc 1101
Db 91 CCAAGTACCCCGAGGAGAGATTCCAAAGATGTAGCCGCGCCACACAGACAGACCTACCC 150
QY 1102 tcttcagaacgaattgacaaacaaattcgtacatctctcgcgcgcatctcagccctgaga 1161
```

```
Db 151 TCTTCAGAACGAATTGACAAACAAATTCGTACATCTTCGAGCGCATCTCAGCCCTGAGA 210
QY 1162 aaggagacatgtatacaagagtagtaacatgtgtgaagcagcaagagaggaactggcagaaaa 1221
Db 211 AAGGAGACATGTAAACAGTAGTAACATGTGTGAAGCAGCAAAAGAGGCACTGGCAGAAAAC 270
QY 1222 aacctgaacctccaaagatggtcgaataagatgtagcttccaatctggattcaatgag 1281
Db 271 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAATCTGGATTCAATGAG 330
QY 1282 gagacttgccgtggtgaataatcatcactggtctctttggagtttgaggtatatacctagatgac 1341
Db 331 GAGACTTGCCGTGGAATCATCACTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 390
QY 1342 ctccagaacagattgagagtagtgaggaacaagccagagctgtgcagatgagtagtaaaaa 1401
Db 391 CTCCAGAAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTAGTACAAA 450
QY 1402 gtcctgatccagttcctgcagaaaaagcgaagaatctagatgcataataacacccctgac 1461
Db 451 GTCCGTGATCCAGTTCTCTGCAGAAAAGCAAGAATCTAGATGCAATTAACCAACCCCTGAC 510
QY 1462 ccaaccacaaatgccagcctgctgcagagctgcaggcacagaacacagtggtgcaggac 1521
Db 511 CCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCACTGGCTGCAGGAC 570
QY 1522 atgacaactatctctatctgcgcagctttaaggaggtctctgcagctccagcctgagggct 1581
Db 571 ATGACAACATCATCTATTCTGGCAGCTTTAAGGAGTCTCTGCAGTTCAGCCTGAGGGCT 630
QY 1582 cttcggcaaatgtagcatgggcacccgtcga 1611
Db 631 CTTCGGCAAAATGTAGCATGGGCACCTCAGA 660

RESULT 15
N90345
ID N90345 standard; DNA; 1101 BP.
AC N90345;
DE 1-NOV-1989 (first entry)
DE Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
DE for immunoglobulin
DE Human lymphocyte receptor for immunoglobulin; cDNA;
DE eukaryotic signal sequence; hypersensitivity; allergy; asthma;
DE BSF-2 leader sequence; plasmid pFc-epsilon-R-1; immunoglobulin E.
FH Key Location/Qualifiers
FT cds 7..642
FT /*tag= a
FT EP-324879-A.
PN 26-JUL-1989.
PD 20-JAN-1988; 100814.
PR 20-JAN-1988; EP-100814.
PA (KISH) Kishimoto T.
PI Schwendenwein R, Sommergruber W, Swetly P;
DR WPI; 89-214148/30.
DR P-PSDB; P90121.
DR Soluble recombinant Fc-epsilon receptor
DR - used for treatment or prophylaxis of local and
DR allergic reactions induced by IgE.
PS Disclosure: fig 3; 24pp; English.
CC Plasmid pBSF2-L8, encoding whole human lymphocyte receptor
CC for immunoglobulin (see P90121). Has BSF-2 leader sequence
CC (c.f. N90344). Used to produce highly bioactive
CC water-soluble FcR. Pref. has interleukin signal sequence.
CC Water-soluble FcR binds IgE, so it is useful for treating
CC hypersensitivity, esp. asthma.
SQ Sequence 1101 BP; 351 A; 227 C; 224 G; 299 T;

Query Match 35.0%; Score 563.6; DB 1; Length 1101;
Best Local Similarity 99.3%; Pred. No. 1.9e-135;
```

Matches 566; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1042 ccagtcaccccccagagagattccaaagatgtagccgccccacacagacagccactcacc 1101
Db 91 CCAGTACCCCCAGGAGAGATTCCAAAGATGTAGCCGCCCCACACAGACACCCACTCACC 150

Qy 1102 tcttcagaaacgaattgacaaacaaattcgtgtacatcctcgcagcgcacatcgcagccctgaga 1161
Db 151 TCCTCAGAACGAATTGACAAACAAATTCGGTACATCCTCGACGGCATCTCAGCCCTGAGA 210

Qy 1162 aaggagacatgtaacaagagtaacatgtgtgaaagcagcaaaagagcagcagcagcaaac 1221
Db 211 AAGGAGACATGTAAACAGAGTAACATGTGTGAAAGCAGCAAAAGAGGCACCTGGCAGAAAAAC 270

Qy 1222 aacctgaaccttccaaagatgctgaaagaaatgagatgcttccaaatctgaattccaatgag 1281
Db 271 AACCTGAACCTTCCAAAGATGGCTGAAAGATGGATGCTTCCAAATCTGGATTCAATGAG 330

Qy 1282 gagacttgcctgttgaaaaatcatcactggtcttttggagtttgaggtatacctagagtac 1341
Db 331 GAGACTTGCCTGGTGAATAATCATCTGGTCTTTTGGAGTTTGAGGTATACCTAGAGTAC 390

Qy 1342 ctccagaaacagatttgagagtagtgaggaaacaaagccagagcgtgtgcagatgagtacaaaa 1401
Db 391 CTCCAGAAACAGATTGAGAGTAGTGAGGACACAGCCAGAGCTGTGCAGATGAGTACAAAA 450

Qy 1402 gtcctgatccagttcctgcagaaaaagcaaaagaaatctagatgcaataaacacccctgac 1461
Db 451 GTCCTGATCCAGTTCCCTGCAGAAAAGGCAAAAGAAATCTAGATGCAATAACCCCTTGAC 510

Qy 1462 ccaaccacaaatgcagcctgtgcagaaagctgcaggcacagaaaccagtggtgcaggac 1521
Db 511 CCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGCAGACAGAACCAAGAGTGCAGGAC 570

Qy 1522 atgacaactcactcattctgcagcagctttaaggagttcctgcagtcagcctgagggct 1581
Db 571 ATGACAACCTCATCTCTCTCGCAGCCTTTAAGGAGTTCCTGCAAGTTCCAGCCTGAGGGCT 630

Qy 1582 ctcggcaaatgtagcatgggcacgcgcga 1611
Db 631 CTTGGCAAAATGTAGCATGGGCACCTCAGA 660

Search completed: August 9, 2000, 09:34:47
Job time: 34153 sec

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	1612	100.0	1612	5	A93715	A93715 Sequence 2
2	1587	98.4	1627	5	A93714	A93714 Sequence 1
3	995	61.7	2066	5	E04823	E04823 CDNA encoding
4	995	61.7	2087	5	E02673	E02673 CDNA encoding
5	995	61.7	3319	9	E12979	E12979 CDNA encoding
6	995	61.7	3319	9	HS1U6R	X12830 Human mRNA
7	993.4	61.6	1486	9	HS1G6EC	X58298 Human mRNA
8	969	60.1	1074	5	AR031384	AR031384 Sequence
c 9	581	36.0	167677	59	AC013588	AC013588 Homo sapiens
c 10	581	36.0	175587	69	AC015889	AC015889 Homo sapiens
11	577.8	35.8	168014	40	AL353649	AL353649 Homo sapiens
12	577.8	35.8	168372	40	AL161629	AL161629 Homo sapiens
13	565.2	35.1	1098	9	HS1UB2R	X04502 Human mRNA
14	565.2	35.1	1102	5	E03737	E03737 CDNA encoding
15	565.2	35.1	1102	10	HUM1L6C	M29150 Human intron
16	565.2	35.1	1113	11	HUM1L6CSF	M54894 Human intron
17	565.2	35.1	1125	9	HUM1FN82B	M18403 Human hybrid
18	565.2	35.1	1139	5	I08633	I08633 Sequence 2
19	565.2	35.1	1161	5	E01616	E01616 CDNA encoding
20	565.2	35.1	1162	5	E01518	E01518 DNA encoding
21	565.2	35.1	1162	5	E01537	E01537 DNA encoding
22	565.2	35.1	1162	5	E02030	E02030 CDNA sequence
23	565.2	35.1	1162	5	E02202	E02202 DNA encoding
24	565.2	35.1	1162	5	E02930	E02930 DNA sequence


```
QY 1141 gacggcatcagccctgagaagagacatgtaacaagataacatgtgtgaagcagc 1200
Db 1141 GACGGCATCTCAGCCCTGAGAAGAGAGACATGTAAACAGTAAACATGTGTAAAGCAGC 1200
QY 1201 aaagaggcaactggcagaaacacacactgaaccttcaaaagatggctgaaaaagatggatg 1260
Db 1201 AAAGAGGCACCTGGCAGAAACACACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGC 1260
QY 1261 ttcaaatcgtgattcaatgagagacttcctggtgaaatacatcaactggtttttggag 1320
Db 1261 TTCCAACTCTGGATTCAATGAGGAGACTTGCCTGGTGAAATAATCATCACTGGCTTTTGGAG 1320
QY 1321 tttaggtatacctagatgacctccagaaacagatttgagagtagtgaggaacaagccaga 1380
Db 1321 TTTGAGGTATACCTAGATGATCCTCAGAAACAGATTTGAGAGTAGTGAGGAACAAGCCAGA 1380
QY 1381 gctgtgcagatgagtacaaaagtccctgatccagttcctgcagaaaaaggaagaatactta 1440
Db 1381 GCTGTGCAGATGAGTACAAAAGTCCCTGATCCAGTTCTCGAGAAAGGCAAGAAATCTTA 1440
QY 1441 gatgcaataaccacccctgacccaacacacaaatgcagcctgctgacgaagctgcaggca 1500
Db 1441 GATGCAATTAACCAACCCCTGACCCACCAACAAATGCCAGCCTGCTGACGAAGCTGCAGGCA 1500
QY 1501 cagaaccagtgctgcagacatgacaaactcatctcattctgcagactttaaggagttc 1560
Db 1501 CAGAACCAGTGCTGCAGACATGACAACTCATCTCATCTCGCAGCTTTAAGGAGTTTC 1560
QY 1561 ctgcagtcagcctgaggctcttcggcaaatgtagcattggcaccagctgcagc 1612
Db 1561 CTGCAGTCCAGCCTGAGGCTCTTCGGCAAAATGTAGCATGGCACCCTGCAGC 1612

RESULT 2
A93714
LOCUS A93714 1627 bp DNA PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9732891.
ACCESSION A93714
VERSION A93714.1 GI:6741885
KEYWORDS
SOURCE
ORGANISM
Rose-John, S.
unidentified.
unclassified.
REFERENCE 1 (bases 1 to 1627)
AUTHORS Rose-John, S.
TITLE CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
JOURNAL Patent: WO 9732891-A 12-SEP-1997;
ANGEWANDTE GENTECNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
FEATURES
Location/Qualifiers
1..1627
/organism="unidentified"
/db_xref="taxon:32644"
34..90
34..1611
/feature="unnamed protein product"
/codon_start=1
/db_xref="GI:6741886"
/translation="MLAVGCALLAALLAALPAGAAALAPRCAPQAEVARGVLTSLPGDSVT
ITCPGEVEDNATVHVLKPAAGSHPSRWAGMRLLRLSVQLHDSGNYSCYRAGR
AGTHLLVDVPPPEPQLSCFRKPSPLSNVVCWGPSTPLATKAVLLVRKTFQNSPAED
FOEPCOYSEOKSCFSCOLAVPEGDSFVIVSMCVASSVSKFSKTOTFGCGIQLPDP
PANTVTAVANPRLSVTWMODPHSWNSFVRLRFLRYRAERSKFTTWMVKLOHH
CVIHDANGLRHVQLRAQBEFGGSEWSEFPMGTWTERSPAPRGSGGSGGS
GGGSVEPVPPEDSKVAAPHROPTLSERIDKQIRVILDIGISALRKETCNKNMCE
SSKALANLNPMAEKDGCFCGFEETCLVKIITGLLEFVLEYLQNRSESE
EQARAVQMSLTVLQFLQKAKNLDAITTPDPTTNASLLTKLQAGNLOWMTHTLIL
RSEKFELOSSLRALRQM"
mat_peptide 91..1608
BASE COUNT 388 a 450 c 481 g 308 t
ORIGIN
```

```
Query Match 98.4%; Score 1587; DB 5; Length 1627;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1612; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 gtcagcagatgagtgtagccgagagagagacatgctggccgtcgcgctgcgctgctg 60
Db 1 GTCAGCAGATGAGTGTAGCCGAGAGAGGAAGCATGCTGGCCGCTCGGCTCGCGCTGCTG 60
QY 61 gctgcccctactgagccgagcgcgagagcgcgctggccccaaagcgcgctgcccgcagga 120
Db 61 GCTGCCCTCTGCTGCCCGCGCGGAGAGCGGCTGGCCCCCAAGGCGCTGCTCGCGCAGGAG 120
QY 121 gttggcaagaggcgtgctgaccagctgctgccaggagagacgctgactctgacctgacc 180
Db 121 GTGGCAAGAGGCGTGTGACCACTGTGCCAGGAGACAGCGTGACTCTGACCTGCCCGGGG 180
QY 181 gttagagccggaagacaataatccactgttcaactgggtgctcaggaaagcgcgctgcag 240
Db 181 GTAGAGCCGGAAGACAATGCCACTGTCTTCACTGGGTGCTCAGGAAGCCGGCTGCAGGCTCC 240
QY 241 caccaccagcagatggctgagcagtggaagagagctgctgactgaagtcgctgagctccc 300
Db 241 CACCCAGCAGATGGCTGGCATGGGAAGAGAGCTCTGCTGAGGTGGTGAGCTGCCAC 300
QY 301 gactctggaactattcatgtaccgggcccggcggccgagctgggactgtgcaactgtctg 360
Db 301 GACTCTGGAACATATTTCATGTACTACGGCGCGCGCGCCAGCTGGGACTGTGCACTTGTCTG 360
QY 361 gtggatgttccccccgagagagccccagctctctctgcttcgaggaagccccctcagcaat 420
Db 361 GTGGATGTTTCCCCCGGAGGAGCCCCAGCTCTCTGCTGCTCCGGGAAGAGCCCGCTTCAGCAAT 420
QY 421 gttgtttgtgagtggtggtcctcgagcaccatccctcaccacaaagcgtgctcttg 480
Db 421 GTTGTGTTGTGAGTGGGGTCTCGAGACACCCCATCTCCACGAAGGCTGTGCTCTTG 480
QY 481 gtgaggaatttcagaaacagtcgcccgaagacttccagagagccgtgcccagttatccccag 540
Db 481 GTGAGGAAGTTTCAGAAACAGTCCGGCCGGAAGACTTCCAGGAGCCGTGCCAGTATTTCCAG 540
QY 541 gagtcccaagaagtctctcctgcagtttagcagtcgccggagggagagacgtcttctacata 600
Db 541 GAGTCCCAAGAAGTTCTCTTCCAGTTAGCAGTCCCGGAGGGAGACAGCTCTTTTCTACATA 600
QY 601 gttgccaatgctgcgccaagtagtgcggagagcaagtgcagcaaaactcaaacctttcag 660
Db 601 GTGTCCATGTGCTGCCAGTAGTGTGCGGAGCAAGTTTCAGCAAAACTCAAACTTTTCAG 660
QY 661 ggtgtggaatcttgagcctgatccgctgccaacatcacagtcactgcccgtggccaga 720
Db 661 GGTGTGGAATCTTGACAGCTGATCCGCTGCCAAACATCACAGTCACTGCCGTGGCCAGA 720
QY 721 aacccccgctggtcagtgtaacctggcaagaccccccaactccttggaaactaatctttctac 780
Db 721 AACCCCCGCTGCTCAGTGTACCTGGCAAGACCCCACTCTCTGGAACACTCATCTTTCTAC 780
QY 781 aaactacggtttgagctcagatatacggtgaacgtcaaaagacattcaacacatgatg 840
Db 781 AGACTACGGTGTTGAGCTCAGATATCGGGCTGAACGGTGAAGAGACATTCAACAACATGGATG 840
QY 841 gtcaagacacctccagcatcactgtgtcatccacgacgctggagcgcctgagggcagctg 900
Db 841 GTCAAGGACCTCCAGCATCACTGTGTATCCAGACGCTTGGAGCGCCTTGAGGCGCTTGAGGCGAGCTG 900
QY 901 gtcagcttcctgtccagagagagttcgggcaagcgagtgagtcgagtcgagtcgagtcgag 960
Db 901 GTCAGCTTCTGTGCCCAGGAGGAGTTTCGGCAAGGCGAGTGGAGCGAGTGGAGCGCGGAG 960
QY 961 gccatgggcagccttggacagaataccagaggtctccagctcga ----- 1005
Db 961 GCCATGGGCAGCCTTTGGACAGAAATCCAGAGTCTCTCCAGCTCGAGGAGGTGAGGTTCT 1020
QY 1006 ggagggtgagggttctggagggtgaggttctgtcgagccagtaaccccccaggaagattcc 1065
```

```
Db 1021 GGAGGTGAGGTTGGAGGTGGAGGTCTCTGAGCCAGTAGACCCAGGAGAGATTC 1080
Qy 1066 aaagatgtagcgcgcacacagacagccactcaccctcttcagacaagaattgacaacaa 1125
Db 1081 AAAGATGTAGCGCGCCACACAGACAGCCACTACCTCTTCAGAACGAATTTGACAAACAA 1140
Qy 1126 attcggtacatcctcgacgcgcatctcagccctgagaaagagacatgttaacaagagtaac 1185
Db 1141 ATTGGGTACATCTCGACGGCATCTAGCCCTGAGAAAGAGAGACATGTAAACAAGTAAC 1200
Qy 1186 atgtgtgaaacagcaagagccactggcagaaacaaacctgaaccttccaaagatggct 1245
Db 1201 ATGTGTGAAAGCAGCAAGAGGCACTGSCAGAAACAACTGAACCTTCCAAAGATGGCT 1260
Qy 1246 gaaaaagatgatcttccaatctggtatcaatgagagacattgcctggtaaaatcatc 1305
Db 1261 GAAAAGATGATGCTTCCCAATCTGGATTCAATGAGGAGACTTGCCTGGTGAATAATCATC 1320
Qy 1306 actggcttttggagtttgaggtatatactagagtacctccagaacagattttgagagtagt 1365
Db 1321 ACTGGCTTTTGGAGTTTGAGGTATACCTAGAGTACCTCCAGAACAGATTTGAGAGTAGT 1380
Qy 1366 gaggaacaaagccagagctgtgcagatgagtacaaaagtccctgatccagttcctgcagaaa 1425
Db 1381 GAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAAGTCTCTGATCCAGTCTCTGCAGAAA 1440
Qy 1426 aaggcaagaatctagatgaataaccacccctgacccaacacaaatgccagcctctg 1485
Db 1441 AAGCAAGAATCTAGATGCAANTAACCCCTGACCCCAACCAACCAAAATGCCAGCCTGCTG 1500
Qy 1486 acgaagctgcaggcacagaaacagtggtgcaggacatgacaaactcatctcttcctgcgc 1545
Db 1501 ACGAAGCTGCAGGCACAGAACCACTGGCTGCAGGACATGACAACTCATCTCTCTCGGC 1560
Qy 1546 agctttaagagttcctgcagtcagcagcctgagggctcttcggcaaatgtagcatgggac 1605
Db 1561 AGCTTTAAGGAGTTCCTGCGATCCAGCTCAGGCTCTCGGCAAAATGATGAGTGGGCAC 1620
Qy 1606 cgtcgac 1612
Db 1621 CGTCGAC 1627

RESULT 3
LOCUS E04823 2066 bp RNA PAT 29-SEP-1997
DEFINITION cDNA encoding interleukin 6 receptor.
ACCESSION E04823
VERSION E04823.1 GI:2173019
KEYWORDS JP 1993091892-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2066)
Kishimoto,C., Hachiman,H. and Yasukawa,K.
IL-6 RECEPTOR DERIVATIVE
Patent: JP 1993091892-A 1 16-APR-1993;
KISHIMOTO CHUZO, CHUGAI PHARMACEUT CO LTD, TOSOH CORP
OS Homo sapiens (human)
PN JP 1993091892-A/1
PD 16-APR-1993
PF 02-OCT-1991 JP 1991255521
PI KISHIMOTO CHUZO, HACHIMAN HIDEO, YASUKAWA KIYOSHI PC
C12P21/02,C07K13/00,C12N5/10,C12N15/12,(C12P21/02,C12N1:91); CC
strandedness: double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT 5'UTR 1..225
```

```
FT CDS 226..1632
FT /product='interleukin 6 receptor' Ft 3'UTR
FEATURES
source 1633..2066.
Location/Qualifiers
1..2066
/organism='Homo sapiens'
/db_xref='taxon:9606'
BASE COUNT 420 a 642 c 615 g 389 t
ORIGIN
Query Match 61.7%; Score 995; DB 5; Length 2066;
Best Local Similarity 100.0%; Pred. No. 2.3e-229;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 catgagtgtagccgaggaggagcatgtgcccgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 67
Db 200 CATGGAGTGGTAGCCGAGGAGGAGCATGTGTGGCGCTCGGCTCGGCTGCTGCTGCC 259
Qy 68 tgcctggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 127
Db 260 TGTGGCGCGCGCGGAGCGCGCTGCCCCAAGCGCTGCCCTGCCCGAGGAGGTGGCAA 319
Qy 128 gagcgtgtgaccagctgtccaggagacagcgtgactctgacctgacctgacctgacctgacct 187
Db 320 GAGCGTGTGTACCACTGTGCCAGGACACAGCGTGACTCTGACCTGCCCGGGGTAGAGC 379
Qy 188 cgaagaacatgcactgttcaactgggtgtcaggaagccggctgcagggtccacccca 247
Db 380 CGGAAGCAATATGCCACTGTTCCTACTGGGTGTTCAGGAAGCGGCTGCAGGCTCCACCCCA 439
Qy 248 qcagatggctgcgcaggaagagcgtgctgctgagtgctgagtgctgagtgctgagtgctgag 307
Db 440 GCAGATGGGTGGCATGGGAGGAGGCTGCTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGT 499
Qy 308 gaaactattcatgtaccggcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 367
Db 500 GAAACTATTCTACCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 559
Qy 368 tccccccgaggagccccagctctcctgttccgggaagagccccccctcagcaattgtgttt 427
Db 560 TTCCCCCGAGGAGCCCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 619
Qy 428 gtgagtggtgctcctcgagcacccccatcctcgacgacaaagcgtgctgctctgtgtgagga 487
Db 620 GTGAGTGGGTCTCTCGAGGACACCCCATCTCTGAGGACAAAGGCTGTGCTCTTGGTGGAGGA 679
Qy 488 agttcagaacagtcgcggccgaagacttccagagcgcgtgccagttatccccagagtgccc 547
Db 680 AGTTTCAGAACAGTCCCGCGCGGAAGACTTCCAGGAGCGGTGCCAGTATTCCAGAGAGTCCC 739
Qy 548 agaagttctcctgccagttagcagtcgccggaggagagacagctcttttatacatagtgcca 607
Db 740 AGAAGTTCTCTCTCGCAGTTAGTAGTCTCCGGAGGAGAGACAGCTCTTCTTACATAGTGCCA 799
Qy 608 tgtgcgtcgccagtagtgcgcggagcaagttcagcaaaactcaaaccttttcaggggtgtg 667
Db 800 TGTGCGTGCAGTAGTGTGCGGAGCAAGTTTCAGCAAACTCAAACTTTTCAGGGTTGTG 859
Qy 668 gaatttcgagcctgatccgcctgccaacatcacagtcactgcctggtggccagaaaccccc 727
Db 860 GAATCTTGACGCTGATCCCGCTTGCCTGCAACATCATACAGTCACTGCGGTGGCCAGAAACCCC 919
Qy 728 gctggctcagtgcaactggagaccccccaactcctggaaactatcttttatacagactac 787
Db 920 GCTGGCTCAGTGTACCTGGCAAGACCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 979
Qy 788 ggttgagctcagatcggtggtgaacggtcaaaagacattcaacaatgagtgatgaag 847
Db 980 GGTTCAGCTCAGATATCGGGCTGAACGGTCAAAAGACATTCAACATTTGATGGTCAAGG 1039
Qy 848 acctccagcatcactgtgtcatccacgacgctggagcgccctgagggcgtgaggtggtgcagc 907
|||||
```

Db 1040 ACCTCCAGCATCTGTGTTCATCAGACGCCCTGGAGCGCCTGAGCAGCTGGTGCAGC 1099
QY 908 ttctgcccagggaggttcggcaaggcgagtgagcagtgagccggagggccatgg 967
Db 1100 TTCTGTCAGGAGGAGTTCGGCAGAGCGAGTGGAGCGAGTGGAGCCCGAGGCCATGG 1159
QY 968 gcacgcttgagacgaatccagaggtctctccagct 1002
Db 1160 GCACGCTTGACAGAAATCCAGGAGTCTCCAGCT 1194

RESULT 4
E02673 2087 bp RNA PAT 29-SEP-1997
LOCUS CDNA encoding human B cell stimulating factor 2 receptor protein.
DEFINITION E02673
ACCESSION E02673
VERSION E02673.1 GI:2170901
KEYWORDS JP 1990288898-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
TITLE Primates; Catarrhini; Hominiidae; Homo.
JOURNAL Kishimoto, C.
HUMAN B CELL STIMULATION FACTOR 2 RECEPTOR PROTEIN
Patent: JP 1990288898-A 1 28-NOV-1990;
KISHIMOTO CHUZO
OS Homo sapiens (human)
PN JP 1990288898-A/1
PD 28-NOV-1990
PF 20-JAN-1989 JP 1989009774
PR 22-JAN-1988 JP 88P 12387, 25-JAN-1988 JP 88P 12599, PR
04-AUG-1988 JP 88P 194885, 14-JAN-1989 JP 89P 7461 PI
KISHIMOTO CHUZO
PC C07K15/06, C07K13/00, C12N5/10, C12N5/20, C12N15/19, C12N15/85, PC
C12P21/02,
PC C12P21/08//A61K37/02, A61K37/02, A61K39/395, C12N15/06,
PC C12P21/02,
PC C12R1:91), (C12P21/08, C12R1:91);
CC strandedness: Doublet;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell type=natural killer cell;
CC *source: cell_line-YT;
CC *source: clone=piBBSF2R;
FH Key Location/Qualifiers
FT CDS 247..1653
FT /product="human B cell stimulating factor 2
FT receptor
FT protein'
FT sig_peptide 247..312
FT mat_peptide 313..1650
FT /product="human B cell stimulating factor 2
FT receptor
FT protein'.
FT Location/Qualifiers
FT 1..2087
FT /organism="Homo sapiens"
FT /db_xref="taxon:9606"

BASE COUNT 425 a 645 c 623 g 394 t
ORIGIN

Query Match 61.7%; Score 995; DB 5; Length 2087;
Best Local Similarity 100.0%; Pred. No. 2.3e-229;
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 catggagtgtagccagaggaagcatgctggccgtcgagtcggcgctggtggtggtgccc 67
Db 221 CATGGAGTGTACCCGAGGAGGAGCATGTCGCCCTGGCGCTGCTGGCTGCC 280

QY 68 tgctggcgccgagcgagcgctggcccccagagcgctgcccctgcccagagtggtgcaa 127
Db 281 TGCTGGCGCGCGGAGCGCGCTGCCCCAGCGCGTCCCTGCGCAGAGGTGGCAA 340
QY 128 gagcgctgctgaccagctctgccaggagacagcgtgactctgacctgcccgggggtagagc 187
Db 341 GAGCGCTGCTGACAGCTCTGCCAGGACAGCGTGACTCTGACCTGCCCGGGGTAGAGC 400
QY 188 cgaagacaatgccactgttcaactgggtgctcaggaagcggctgagggctccacaccca 247
Db 401 CGGAAGACAATGCCACTGTTCACCTGGGTGTCAGGAAGCGGCTGCAAGGTCACACCCCA 460
QY 248 gcagatggcgctggcatgggaagagcgctgctgctgaggtcggtgacgtccacagactcg 307
Db 461 GCAGATGGCGTGGCATGGGAAGAGGCTGTCTGCTAGGTGGTGCAGCTCCACGACTGTG 520
QY 308 gaaactattcatgctaccggggcgcccgagctgggactgtgcaactgtctggtggtgatg 367
Db 521 GAAACTATTTCATGCTACCGGGCGCGCCAGCTGGGACTGTGCACCTTGTCTGGTGGATG 580
QY 368 ttccccccgaggagccccagctctctctcgggaagagccccctcagaatgttttt 427
Db 581 TTCCCCCGAGAGCCCCAGCTCTCTCTGCTTCCGGAAGAGCCCCCTCAGCAATGTTGTT 640
QY 428 gtgagtggtgctctcgagcacccatccctcgacacaaaggtgtgctcttggtagga 487
Db 641 GTGAGTGGGTCTCTCGGAGCACCCCATCCCTGACGACAAAGGCTGTCTCTTGTGTGAGGA 700
QY 488 agttcagaacagtcgccggcggaagacttccagagcgctgcccagtgattccccagagtc 547
Db 701 AGTTTTCAGAACAGTCCGCGCGAAGACTTCCAGGAGCGCTGCCAGTATTTCCAGGAGTCCC 760
QY 548 agaagttctctgccagttgagcagtcgccggagggagagcagctctttctacatagtcaca 607
Db 761 AGAAGTTCCTCTGCCAGTTAGCAGTCCCGGAGGAGAGAGCTCTTTTACATAGTGTCCA 820
QY 608 tgtgcgtcgccagtagtgcgggagcaagttcagcaaaactcaaacctttcaggggtgtg 667
Db 821 TGTGCGTGGCGAGTAGTGTGGGAGCAAGTTTCAGCAAAACTCAAACTTTTCAGGGGTGTG 880
QY 668 gaattctgagcctgatccgctgcccacatcacagtcactgcccgtggccagaaaccccc 727
Db 881 GAATCTTGCAGCCTGTATCCGCCCTGCCAACATCACAGTCACTTGGCGTGGCAGAAACCCCC 940
QY 728 gctggctcagtgtaacctggcaagacccccactcctggaactcatttctacagactac 787
Db 941 GCTGGCTCAGTGTCACTGGCAGACACCCCACTCCTCTGGAATCATCTTTCTACAGACTAC 1000
QY 788 ggttgagctcagatatcggtgaaacggtcaagacatcacacatgagtggtcaagg 847
Db 1001 GGTTTGAGCTCAGATATCGGGCTGAACGGTCAAGAGATTCAACATGATGGATGTCAAGG 1060
QY 848 acctccagcatcactgtgtcatccacgacgcctgagcgctgagcgctgagcgctggtgagc 907
Db 1061 ACCTCCAGCATCACTGTGTCTATCCAGCGCTTGGAGGGCTTGGAGCAGCTGTGTGCAGC 1120
QY 908 ttctgcccagggaggttcggcgcaaggcgagtgagtcgagtcgagcccgagggccatgg 967
Db 1121 TTCTGTCAGGAGGAGTTCGGGCAAGGCGAGTGGAGCGAGTGGAGCCCGAGGCCCATGG 1180
QY 968 gcacgcttgagacgaatccagaggtctccagct 1002
Db 1181 GCACGCTTGGACAGAAATCCAGGAGTCTCTCCAGCT 1215

RESULT 5
E12979
LOCUS CDNA encoding human interleukin-6 receptor.
DEFINITION E12979
ACCESSION E12979
VERSION E12979.1 GI:3251803
KEYWORDS JP 1997118623-A/1.
SOURCE Homo sapiens.


```
QY 94 gccccaggcgctgccctgcgcaggaggtggaagagcgctgtgaccagctgtgccagga 153
Db 61 GCCCAAAGGGCGTCCCTGCGCAGAGGTTGGCAAGAGCGTGTGACCAAGTCTCCAGGA 120
QY 154 gacagctgactctgacctgcccgggggtagagccggaagaacatgccaactgttcaatgg 213
Db 121 GACAGCGTGACTCTGACTGCTCCCGGGGTAGAGCGCGGAAGACAATGCCATGTTCACTGG 180
QY 214 gtgctcaggaagccggctgcaggctcccccacccagcagatgggctgcatgggaagagg 273
Db 181 GTGCTCAGGAAGCGGCTGCAGGCTCCACCCACAGCAGATGGGTGCGATGGGAAGAGG 240
QY 274 ctgctgctgaggctggtgcagctccacgactctggaactattcatctaccgggcccgc 333
Db 241 CTGCTGCTGAGGTGGTGCAGTCCACGACTCTGGAATATTTCATGCTACCGGGCCGCG 300
QY 334 cgcacagctgggactgtgactgtgctggtggtggttccccccagagggccccagctctcc 393
Db 301 CGCCACGCTGGGACTGTGCACTTGTCTGGTGGATGTTTCCCGCAGAGAGCCCCAGCTCC 360
QY 394 tgcctccggaagagccccctcagcaatgttgttgtagtgggtcctcgagagcacccca 453
Db 361 TGCTCCGGAAGAGCCCCCTCAGCAATGTGTGTGAGTGGGTCTCGAGGACCCCA 420
QY 454 tcctgacgacaaaggctgtctctgtgtgaggaagtttcagaacagtcgggcccgaagac 513
Db 421 TCCCTGACGACAAAGGCTGTGCTTGTGTGAGGAAGTTTCAGAACAGTCCGGCCGAAGAC 480
QY 514 ttccaggagccgtgcagatattccagagatccagaaagtctctcaggttagcagtc 573
Db 481 TTCAGAGAGCCGTGCCAGTATCCACAGAGTCCACAGAAAGTTCTCTCCCAAGTAGCAGTC 540
QY 574 ccggaggagacagctcttctacatagttccatgtgcctgcctccagtagtcgggagc 633
Db 541 CCGGAGGAGACAGACTCTTTCTACATAGTGTCCATGTGCGTCCGACATGTGCGGAGC 600
QY 634 aagttcagcaaaactcaaaacctttcagggtgtggaattcttgagcctgacccgctgcc 693
Db 601 AAGTTCAAGAAAACATAAACCCTTTCAGGGTTGTGGAATCTTGCAGCCTGATCCGCTGCC 660
QY 694 acatcacagctactgcgtgcccagaaaaaccccgctgctcaggtgcactgtgcaggaac 753
Db 661 AACATCACAGTCACTGCGGTGGCCAGAAAACCCCGCTGGCTCAGTGTGCACTGGCAAGAC 720
QY 754 cccactcctggaaactcatcttctacagactcaggtttgagctcagatcaggtcga 813
Db 721 CCCCACTCTCGGAACACTCATCTTCTACAGACTACGGTTTACGCTCAGATATCGGGCTGAA 780
QY 814 cgtcaagagacattcaacaacatggatgggtcaaggacctccagcatcactgtgtcatccac 873
Db 781 CGGTCAAAAGACATTCAACAACATGGATGGTCAAGGACCTCCAGCATCACTGTGTATCCAC 840
QY 874 gacgctggagcgccgtgagcgacgtggtgcagcttcgtccagagggaggttcgggcaa 933
Db 841 GAGCGCTTGGAGCGGCTGTGAGCGACGTGGTGCAGCTTGTGTCGCCAGGAGAGTTCGGGCAA 900
QY 934 ggcgagtgagcagtgagccgagcccatgggcacgccttgagcagacgaatccagaggt 993
Db 901 GGGGAGTGGAGCGAGTGGAGCCCGGAGGCCATGGGCACGCTTGGACAGAAATCCAGGAGT 960
QY 994 cctccagct 1002
Db 961 CCTCCAGCT 969
RESULT 9
LOCUS AC013588/c
DEFINITION Homo sapiens clone RP11-8B23, WORKING DRAFT SEQUENCE, 15 unordered
pieces.
ACCESSION AC013588
VERSION AC013588.3 GI:7329375
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
```

SOURCE
ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 167677)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens, clone RP11-8B23

Unpublished

2 (bases 1 to 167677)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouknight,B.,
Cooke,P., Castle,A., Colangelo,M., Collins,S., Collamore,A.,
Crook,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferrelira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galaan,J., Gardyna,S., Grant,G., Hagos,B., Harford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karas,A., Klein,J.,
Lechoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Rhomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 26, 2000 this sequence version replaced gi:6514000.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2963

Center clone name: 8.B.23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 159183 bases at least Q40

Consensus quality: 163476 bases at least Q30

Consensus quality: 164920 bases at least Q20

Insert size: 165000; agarose-fp

Insert size: 166277; sum-of-contigs

Quality coverage: 4.2 in Q20 bases; agarose-fp

Quality coverage: 4.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 15 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1

* 2090: contig of 2090 bp in length

* 2091 2190: gap of 100 bp

* 2191 4992: contig of 2802 bp in length

* 4993 5092: gap of 100 bp

* 5093 7384: contig of 2292 bp in length

* 7385 7484: gap of 100 bp

* 7485 11034: contig of 3550 bp in length

* 11035 11134: gap of 100 bp

* 11135 15041: contig of 3907 bp in length

* 15042 15141: gap of 100 bp

* 15142 21265: contig of 6124 bp in length

* 21266 21365: gap of 100 bp

* 21366 28896: contig of 7531 bp in length

* 28897 28996: gap of 100 bp

* 28997 34811: contig of 5815 bp in length


```

QY 788 ggtttgagctcagatcggtggaacggtcaaacgattcaaacatggtggtcaagg 847
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84669 GGTTTGAGCTTTGATACCTGGCTAAATAGTCAAAAATGTTCAATACATGATGGCCAAAG 84610
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 848 acctcagatcactgtgtcattccacagcgcctgagcgccctgagggcactggtgacgc 907
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84609 ATCTCAACATCAGTGTGTCATTCACAAACACCTGGAAAGGCATGAGCCACACAGCAGC 84550
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 908 ttctgtccaggagaggttcgcgaaggcagtgagtgagtgagtgagtgagtgagtgagtgag 967
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84549 TTCAGCCCCAGAGGAGCTGGGGCAGAGCTTGTGAAGTAAGTGGAGCCAGAGGTCATGG 84490
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 968 gcacgccttgacagaatccaggagtcctccagct 1002
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84489 GAACCTTTGGGAGACTCCAGGAGTCTCTCCAGCT 84455
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
AL353649/c
LOCUS
DEFINITION
Homo sapiens chromosome 9 clone RP11-30P16, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION
AL353649
VERSION
AL353649.1 GI:7635196
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 168014)
Plumb,B.
Direct Submission
Submitted (20-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba30P16
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 153632 bases at least Q40
Consensus quality: 158903 bases at least Q30
Consensus quality: 162319 bases at least Q20
Insert size: 165814; sum-of-contigs
Insert size: 156860; agarose-fp
Quality coverage: 3.85x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'unfinished' sequence. It currently * consists of
23 contigs. The true order of the pieces is * not known and their
order in this sequence record is * arbitrary. Where the contigs
adjacent to the vector can * be identified, they are labelled with
'clone_end' in the * feature table. Some order and orientation
information * can tentatively be deduced from paired sequencing
reads * which have been identified to span the gap between two *
contigs. These are labelled as part of the same *
'fragment_chain', and the order and relative orientation * of the
pieces within a fragment_chain is reflected in * this file. Gaps
between the contigs are represented as * runs of N, but the exact
sizes of the gaps are unknown. * This record will be updated with
the finished sequence as * soon as it is available and the
accession number will be * preserved.
1 14912 contig of 14912 bp in length; fragment_chain 1
* 15013 17004 contig of 1992 bp in length; fragment_chain 1 *
17105 33287 contig of 16183 bp in length; fragment_chain 1 *
33388 38481 contig of 5094 bp in length; fragment_chain 1 *
38582 44792 contig of 6211 bp in length; fragment_chain 1 *

```

```

44893 47024 contig of 2132 bp in length; fragment_chain 2 *
47125 58864 contig of 11740 bp in length; fragment_chain 2 *
58965 60033 contig of 1069 bp in length
60134 61190 contig of 1057 bp in length
* 61291 69752 contig of 8462 bp in length
69853 70859 contig of 1007 bp in length
* 70960 72257 contig of 1298 bp in length
72358 73398 contig of 1041 bp in length
* 73499 74668 contig of 1170 bp in length
74769 82676 contig of 7908 bp in length
* 82777 101516 contig of 18740 bp in length
101617 102936 contig of 1320 bp in length
* 103037 114706 contig of 11670 bp in length
114807 115872 contig of 1066 bp in length
* 115973 117049 contig of 1077 bp in length
117150 136261 contig of 19112 bp in length
* 136362 160914 contig of 24553 bp in length
161015 168014 contig of 7000 bp in length.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
FEATURES
Source
Location/Qualifiers
1..168014
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-30P16"
/clone_lib="RPC1-11.1"
1..14912
/notes="assembly_fragment:00024"
fragment_chain:1
clone_end:SP6
vector_side:left
15013..17004
/notes="assembly_fragment:01568"
fragment_chain:1
17105..33287
/notes="assembly_fragment:01118"
fragment_chain:1
33388..38481
/notes="assembly_fragment:00793"
fragment_chain:1
38582..44792
/notes="assembly_fragment:00753"
fragment_chain:1
44893..47024
/notes="assembly_fragment:00142"
fragment_chain:2
47125..58864
/notes="assembly_fragment:01555"
fragment_chain:2
58965..60033
/notes="assembly_fragment:00237"
60134..61190
/notes="assembly_fragment:00342"
61291..69752
/notes="assembly_fragment:00541"
69853..70859
/notes="assembly_fragment:00650"
70960..72257
/notes="assembly_fragment:00681"
72358..73398
/notes="assembly_fragment:00698"
73499..74668
/notes="assembly_fragment:00805"
74769..82676
/notes="assembly_fragment:00822"
82777..101516
/notes="assembly_fragment:00827"
101617..102936
/notes="assembly_fragment:00912"
103037..114706

```


misc_feature 547..555
/note="pot. N-glycosylation site"
misc_feature 1072..1077
/note="put. polyA signal"
polyA_site 1098
/note="polyA site"
BASE COUNT 333 a 237 c 226 g 302 t
ORIGIN

Query Match 35.1%; Score 565.2; DB 9; Length 1098;
Best Local Similarity 99.5%; Pred. No. 7.8e-126;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 ccaagtacccccaggagaagattccaaagatgtagccgccccacacagacagcactcacc 1101
DB 118 CCAGTACCCCGAGGAGAAATTCCAAAGATGTAGCGCGCCACACAGACAGCCACTCACC 177
QY 1102 tcttcagaacgaattgacaaaaaaatcgggtacatctctcgacgggaatctcagccctgaga 1161
DB 178 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCGACGGCATCTCAGCCCTGAGA 237
QY 1162 aaggagacatgtaaacagagttaacatgtgtgaagcagcaagagagcactggcagaaaaac 1221
DB 238 AAGGAGACATGTAAACAGAGTAACATGTGTGAAGCAGCAAAAGAGGACACTGGCAGAAAAAC 297
QY 1222 aaactgaaccttccaaagatgctgaaaaaagatggatgcttccaatcttgattcaatgag 1281
DB 298 AACCTGAACCTTCCAAAGATGGCTGNAAGAAGATGGATGCTTCAATCTGGATTCAATGAG 357
QY 1282 gagacttgctggtgaaaaatcatcactggtctctttggagtttgaggtatataccttagagtag 1341
DB 358 GAGACTTGCTGGTGAATAATCATCACTGTCTCTTTGGAGTTTGAGGTATACCTAGAGTAC 417
QY 1342 ctcccgaaacagatttgagagtagtgaggaaacagccagagctgtgcagatgtagtacaata 1401
DB 418 CTCGAGAACAGATTTGAGAGTAGTGAGGAACCAAGCCAGAGCTGTGCAGATGATGACAAAA 477
QY 1402 gtccctgatccagttctcagaaaaagcaagaatcttagatgcaataaccacccctgac 1461
DB 478 GTCTGTATCCAGTTCTCGAGAAAAGGCAAGAATCTAGATGCAATACCAACCCCTGAC 537
QY 1462 ccaaccacaaaatgccagcctgctgacgaagctgcagggcacagaaccagtggtctgcaggac 1521
DB 538 CCAACCACAAAATGCCAGCCTGTGACGAAGCTGCAGGCACAGAACCCAGTGGCTGCAGGAC 597
QY 1522 atgacaactcatctattctgcgcagctttaaggagtttaaggagttcctgcagtcacgctgagggct 1581
DB 598 ATGACAACCTCATCTATTCTGGCGAGCTTTAAGGAGTTCCTGCAGTCCAGCCTGAGGGCT 657
QY 1582 ctccggcaaatgtagctggccaccgtcga 1611
DB 658 CTTCCGCAATGTAGCATGGGCACCTCAGA 687

RESULT 14
E03737
LOCUS E03737 1102 bp RNA PAT 29-SEP-1997
DEFINITION CDNA encoding human B-cell differentiation factor.
ACCESSION E03737
VERSION E03737.1 GI:2171952
KEYWORDS JP 1992169599-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1102)
Yasuda,H., Nagase,K., Kawai,M., Fukuhara,K. and Matsui,Y. .
VARIANT HUMAN BCF
TITLE
JOURNAL Patent: JP 1992169599-A 1 17-JUN-1992;
AJINOMOTO CO INC
COMMENT OS Homo sapiens (human)
PN JP 1992169599-A/1

PD 17-JUN-1992
PF 30-OCT-1990 JP 1990290704
PI YASUEDA HISASHI, NAGASE KAZUO, KAWAI MISAHO, FUKUHARA KENICHI,
PI MATSUI YUTAKA
PC C07K13/00,C12N15/24,C12P21/02//A61K37/02,A61K37/02,A61K37/02,
PC (C12P21/02,
PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
FH Key
FT 5'UTR <1..35
FT CDS 36..674
FT /product='B-cell differentiation factor' FT
FT sig_peptide 36..119
FT /product='signal peptide of B-cell FT
FT differenceciation factor'
FT mat_peptide 120..671
FT /product='B-cell differentiation factor' FT
FT 3'UTR 675..1102.
FEATURES
source
Location/Qualifiers
1..1102
/organism='Homo sapiens'
/db_xref='taxon:9606'
BASE COUNT 336 a 238 c 226 g 302 t
ORIGIN

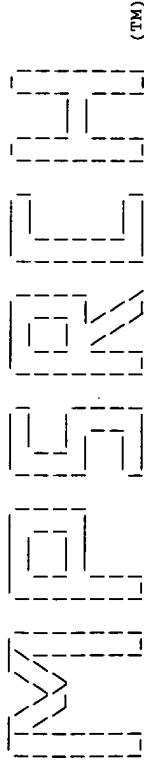
Query Match 35.1%; Score 565.2; DB 5; Length 1102;
Best Local Similarity 99.5%; Pred. No. 7.8e-126;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 ccaagtacccccaggagaagattccaaagatgtagccgccccacacagacagcactcacc 1101
DB 120 CCAGTACCCCGAGGAGAAATTCCAAAGATGTAGCGCGCCACACAGACAGCCACTCACC 179
QY 1102 tcttcagaacgaattgacaaaaaaatcgggtacatctctcgacggcatctcagccctgaga 1161
DB 180 TCTTCAGAACGAATTGACAAACAAATTCGGTACATCTCTGACGGCATCTCAGCCCTGAGA 239
QY 1162 aaggagacatgtaaacagagttaacatgtgtgaagcagcaaaagagcactggcagaaaaac 1221
DB 240 AAGGAGACATGTAAACAGAGTAACATGTGTGAAGCAGCAAAAGAGGACACTGGCAGAAAAAC 299
QY 1222 aaactgaaccttccaaagatggctgaaaaagatggatgtcttcccaatctgagtttaaatgag 1281
DB 300 AACCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAATCTGGATTCAATGAG 359
QY 1282 gagacttgctggtgaaaaatcatcactggtctttggagtttgaggtatataccttagagtag 1341
DB 360 GAGACTTGCTGTGTGAAATTCATCTGCTGCTTTTGGAGTTTGAGGTATACCTAGAGTAC 419
QY 1342 ctccagaacagatttgagagtagtgaggaacaagcagagcgtgtgcagatgagtagacaaa 1401
DB 420 CTCACAGACAGATTTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAA 479
QY 1402 gtccctgatccagttcctgcagaaaaagcagaaagaatagatgcaataaccacccctgac 1461
DB 480 GTCTGTATCCAGTTCTCTGCAGAAAAAGGCAAGAATCTAGATGCAATCAATACCCCTGAC 539
QY 1462 ccaaccacaaaatccagcctgctgacgaagcactgaggaacacagacagcactggctgcagag 1521
DB 540 CCAACCACAAAATGCCAGCCTGCTGACGAAGCTGCAGGACACAGAACCAAGTGGCTGCAGGAC 599
QY 1522 atgacaactcatctattctgcgcagctttaaggagtttctcagtcagtcacgctgagggct 1581
DB 600 ATGACAACCTCATCTCATCTGCGCAGCTTTAAGGAGTTCCTGCAGTCCAGCCTGAGGGCT 659
QY 1582 ctccggcaaatgtagctgggcaccgtcga 1611
DB 660 CTTCCGCAATGTAGCATGGGCACCTCAGA 689

RESULT 15
LOCUS HUMIL6C 1102 bp mRNA PRI 06-JAN-1995
DEFINITION Human interleukin 6 (B-cell stimulatory factor-2) mRNA, complete cds.
ACCESSION M29150.1 GI:186349
VERSION B-cell stimulatory factor-2; BSF-2; cytokine; interleukin 6;
KEYWORDS transmembrane glycoprotein.
SOURCE Human cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1102)
AUTHORS Tonouchi, N., Miwa, K., Karasuyama, H. and Matsui, H.
TITLE Deletion of 3' untranslated region of human BSF-2 mRNA causes
stabilization of the mRNA and high-level expression in mouse NIH3T3
cells
JOURNAL Biochem. Biophys. Res. Commun. 163 (2), 1056-1062 (1989)
MEDLINE 89391958
FEATURES
Location/Qualifiers
1..1102
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="7p21-p14"
36..674
/gene="IL6"
36..674
/gene="IL6"
/note="interleukin 6"
/codon_start=1
/db_xref="GDB:G00-120-748"
/protein_id="AAA59154.1"
/db_xref="GI:307063"
/translation="MNSFSTSAFGPVAFSGLLLVLPAAFPAPVPPEEDSKDVAAPHR
QPTSSRIDQRIYILDGILSKRCKNSKMSKEALNNLNLPKAEKDGCF
QSGNEETCLVKIITLLEFVLYLEIQNRFESSEQARAVQMSTKVLIOFLQKKAKN
LDAITTPDTTNSLTKLQAQNWQLQDMTTHILRSFKFEFLQSLRLRQM"
BASE COUNT 336 a 238 c 226 g 302 t
ORIGIN
Query Match 35.1%; Score 565.2; DB 10; Length 1102;
Best Local Similarity 99.5%; Pred. No. 7.8e-126;
Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1042 ccagtacccccaggagaagattccaagatgtacccgccccacacagacagccactcacc 1101
Db 120 CCAGTACCCCCAGGAGAGATTCCAAAGATGTAGCCGCCCCACACAGACAGCCACTCACC 179
QY 1102 tcttcagaacgaattgacaacaattcgttacatcctcgacgcgcattctcagccctgaga 1161
Db 180 TCTTCAGAACGAATTGACAAACAATTTCGGTACATCTCTGACGGGCATCTCAGCCCTGAGA 239
QY 1162 aaggagacatgtaacaagagtaacatgtgtgaaagcagcaaaaggcagcactggcagaaaa 1221
Db 240 AAGGAGACATGTAAACAGAGTACATGTGTAAAGACAGCAAAAGAGGCACCTGGCAGAAAA 299
QY 1222 aacctgaacctccaaagatggctgaaaagatggatgcttccaatctggtattcaatgag 1281
Db 300 AACCTGAACCTTCCAAAGATGGCTGAAAAGATGGATGCTTCCAAATCTGGATTCAATGAG 359
QY 1282 gagacttgcctggtgaaaatcactcgtgttttggagtttgaggtataggtataggtac 1341
Db 360 GAGACTTGCTGTGGTGAATAATCATCAGTGGTCTTTTGGAGTTGAGGTATACCTAGAGTAC 419
QY 1342 ctccagaaacagatttgagtagtgaggaacaagccagagctgtgcagatgagtacaaaa 1401
Db 420 CTCAGAACAGATTGAGAGTAGTGAGGAACAAGCCAGAGCTGTGCAGATGAGTACAAAA 479
QY 1402 gtctgatccagttccttcgcagaaaaaggcaagaatctagatgaataaccacctgac 1461

Db 480 GTCTGTATCCAGTTCTCTCAGAAAAAGCAAGAATCTAGATGCAATAACCACTCCCTGAC 539
QY 1462 ccaaccacaaatgccagcctgtgacgaagctgcaggcacagaaacagtggtgctgcaggac 1521
Db 540 CCAACCAAAATGCCAGCCTGCTGACGAAGCTGCAGGCACAGAACCACTGGCTGCAGGAC 599
QY 1522 atgacaaatcattcattctgcgaagctttaagagagttcctgcagtcagcctgagggct 1581
Db 600 ATGACAACTCATCTCATTTCTGCGCAGCTTTAAGGAGTTCTCTGCAGTCCAGCTGAGGGCT 659
QY 1582 ctccggcaaatgtagcatggcaccgtcga 1611
Db 660 CTTCCGGCAAAATGTAGCATGGGCACCTCAGA 689

Search completed: August 9, 2000, 07:07:22
Job time: 62356 sec



Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:16:47 2000; MasPar time 40.07 Seconds
Tabular output not generated. 899.809 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.pep
Perfect Score: 3771
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILSPKFEFLQSSLRALRQM 520

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 50.078; Variance 91.622; scale 0.547

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1320	35.0	440	11	Q00343	INTERLEUKIN 6 RECEPTOR	1.90e-260
2	1239	32.9	209	6	Q97540	INTERLEUKIN-6 (FRAGMEN	6.06e-242
3	814	21.6	209	6	Q28819	INTERLEUKIN 6 (FRAGMEN	7.29e-146
4	810	21.5	205	6	Q28747	INTERLEUKIN 6 (FRAGMEN	5.70e-145
5	804	21.3	208	6	Q9XT80	INTERLEUKIN 6 PRECURSO	1.25e-143
6	748	19.8	160	6	Q97535	INTERLEUKIN-6 (FRAGMEN	3.66e-131
7	725	19.2	207	6	Q28403	INTERLEUKIN 6 (FRAGMEN	4.64e-126
8	539	14.3	210	11	Q9WVQ8	IL-6 (FRAGMENT)	2.71e-85
9	415	11.0	372	11	Q88507	CILIARY NEUROTROPHIC F	7.68e-59
10	406	10.8	432	11	Q64385	INTERLEUKIN-11 RECEPTO	5.91e-57
11	401	10.6	432	11	P70225	INTERLEUKIN-11 RECEPTO	6.57e-56
12	397	10.5	66	6	Q18796	INTERLEUKIN 6 RECEPTO	4.50e-55
13	337	10.5	422	4	Q16542	INTERLEUKIN-11 RECEPTO	4.50e-55
14	381	10.1	94	6	Q62775	INTERLEUKIN 6 (FRAGMEN	9.60e-52
15	329	8.7	101	11	O55041	INTERLEUKIN 6 (FRAGMEN	4.52e-41
16	252	6.7	204	14	O40918	ORF K2.	7.97e-26
17	252	6.7	204	14	Q98823	INTERLEUKIN-6 HOMOLOG	7.97e-26
18	202	5.4	422	4	O75462	CYTOKINE-LIKE FACTOR-1	1.83e-16
19	182	4.8	228	11	O35228	CYTOKINE RECEPTOR-LIKE	6.77e-13
20	180	4.8	581	6	O46561	PROLACTIN RECEPTOR LON	1.52e-12

21	179	4.7	296	6	O18880	PROLACTIN RECEPTOR SHO	2.27e-12
22	168	4.5	229	4	Q75269	HUMAN CYTOKINE RECEPTO	1.78e-10
23	163	4.3	229	4	O14213	CYTOKINE RECEPTOR PREC	1.25e-09
24	161	4.3	346	13	Q93404	PROLACTIN RECEPTOR (FR	2.70e-09
25	151	4.0	335	6	P79203	PROLACTIN RECEPTOR (FR	1.21e-07
26	142	3.8	206	4	Q16354	PROLACTIN RECEPTOR (FR	3.37e-06
27	144	3.8	316	11	Q35545	INTRON 5-INSERTED FORM	1.62e-06
28	130	3.4	217	6	O46386	PROLACTIN RECEPTOR (FR	2.43e-04
29	128	3.4	266	5	P91608	LIM DOMAIN PROTEIN BX	4.85e-04
30	130	3.4	329	6	Q9XSQ5	INTERLEUKIN 12 P40 SUB	2.43e-04
31	130	3.4	625	6	Q9XS92	PROLACTIN RECEPTOR PRE	2.43e-04
32	129	3.4	895	11	O62960	LEPTIN RECEPTOR.	3.43e-04
33	124	3.3	194	6	O02708	GLYNULOCYTE COLONY-STI	1.90e-03
34	124	3.3	229	6	Q28206	ERYTHROPOIETIN RECEPTO	1.90e-03
35	124	3.3	229	6	Q27950	ERYTHROPOIETIN RECEPTO	1.90e-03
36	126	3.3	874	11	P97378	INTERLEUKIN 12 RECEPTO	9.65e-04
37	123	3.3	1165	6	O02671	TRANSMEMBRANE LEPTIN R	2.67e-03
38	119	3.2	796	13	Q91287	FIBROBLAST GROWTH FACT	1.01e-02
39	122	3.2	862	4	Q99665	IL-12 RECEPTOR BETA2.	3.74e-03
40	122	3.2	881	13	O57519	GPI30P1.	3.74e-03
41	120	3.2	1250	11	O88971	CDO.	7.29e-03
42	121	3.2	1571	4	O60469	DOWN SYNDROME CELL ADH	5.22e-03
43	121	3.2	1896	4	O60468	DOWN SYNDROME CELL ADH	5.22e-03
44	118	3.1	1240	4	O14631	CDO.	1.41e-02
45	118	3.1	5198	5	O76518	HEMICENTIN PRECURSOR.	1.41e-02

ALIGNMENTS

RESULT 1
ID Q00343 PRELIMINARY; PRT; 440 AA.
AC Q00343;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN 6 RECEPTOR, ALPHA PRECURSOR
DE (MUTANT INTERLEUKIN-6 RECEPTOR).
GN IL6RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE; 90278354.
RA SUGITA T., TOSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO T.,
RA KISHIMOTO T.;
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomagenesis.";
RL J. Exp. Med. 171:2001-2009(1990).
CC -!- MISCELLANEOUS: THIS PROTEIN IS A ABNORMAL INTERLEUKIN-6 RECEPTOR.
CC IN THE CDNA ENCODING THE ABNORMAL INTERLEUKIN-6 RECEPTOR THE
CC REGION CORRESPONDING TO ITS INTRACYTOPLASMIC DOMAIN WAS REPLACED
CC WITH A LONG TERMINAL REPEAT OF THE INTRACISTERNAL A PARTICLE (IAP)
CC GENE. A MEMBER OF THE ENDOGENOUS PRORETROVIRAL-LIKE ELEMENTS
CC PRESENT IN THE GENOME OF MUS MUSCULUS.
DR EMBL; X51976; CAA36238.1; -.
DR PIR; J01044; J01044.
DR HSSP; P14787; IAN3.
DR MGD; MGI:105304; IL6ra.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; ig; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 440 MUTANT INTERLEUKIN-6 RECEPTOR.
FT DOMAIN 1 385 INTERLEUKIN-6 RECEPTOR PORTION.
FT DOMAIN 20 357 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 43 36 IG-RELATED.
FT TRANSMEM 358 385 POTENTIAL.
FT DOMAIN 386 440 IAP PORTION.
FT DOMAIN 386 440 INTRACELLULAR (POTENTIAL).
FT DISULFID 47 92 POTENTIAL.

```
FT CARBOHYD 32 32 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 150 150 POTENTIAL.
SQ SEQUENCE 440 AA; 47901 MW; 8587B93 CRC32;

Query Match 35.0%; Score 1320; DB 11; Length 440;
Best Local Similarity 55.1%; Pred. No. 1.90e-260;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLTVCCTLLVALLAALVALVGLSCRALEAVANGIVTSLPGATVILICPGKEAAGNVTIHW 60
Qy 1 MLVACALLAALLAAGAAALAPRCPAQEVARGVLTSLPGSDSVLTCTCPGPEPDNATVHW 60
Db 61 VY----SGSQNRWTTTNTLVLDVQLSDGTGCLNDHLVGTVPVLLVDVPEEPKLS 116
Qy 61 VLRPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPOLS 120
Db 117 CFRKNPLVNAICEWRPSPTPTKAVLFARKINTNGSKDFQVPCQYSQLKSFSCOVE 176
Qy 121 CFRKSPLSNVVCWGPSTPSLTITKAVLLVRKFQNSPAE-DFQEPQCYQSQSKFSCOLA 179
Db 177 ILEGDKVYHIVSLCVANSVSGSKSHNEAFSLKMWQDPDPANLVSAIPGRPLKYSWQ 236
Qy 180 VPEGSSYIIVSMCVASSVSGSKFTQTFQCGILQPPPPANITVTAVRNPLSVTWQ 239
Db 237 HPETWDPYSYLLQFLQRPVWVSKEFTVLLLPVAVQCYQVIHDALRGVHVQVVRGKEELD 296
Qy 240 DPHSNWSFYRLRELRYRAERSKFTTVMVKDQLQHCVIHDAMSLGRHVVLQRAQBEFG 299
Db 297 LGQWSEWSPEVTGPTWIAEPTTFA 321
Qy 300 QGEWSEWSPEAMGTPW-TESSRPA 323

RESULT 2 PRELIMINARY; PRT; 209 AA.
ID O97540;
AC O97540;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nancymaeae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
RN
RP SEQUENCE FROM N.A.
RA ECEVERRY S.J., HERNANDEZ E., MORENO A., PATAROTO M.E., MURILLO L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014510; AAD01536.1; -.
DR HSP; P05231; IALU.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1 1
FT NON_TER 209 209
SQ SEQUENCE 209 AA; 23406 MW; 99D77053 CRC32;

Query Match 32.9%; Score 1239; DB 6; Length 209;
Best Local Similarity 97.2%; Pred. No. 6.06e-242;
Matches 176; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 29 PVPFGDSKEVAAPNROPLASTEQIDKIRYILDIGISALRKETCNKSNMCESSKEALAE 88
Qy 337 PVPFGDSKDVAAHPHQPLTSRERIDKQIRYILDIGISALRKETCNKSNMCESSKEALAE 396
Db 89 NLNPKMAEDGCGFQSGFNEETCLVKITGLLEFEVYLEYLNRFESSEQARAVQMSTK 148
Qy 397 NLNPKMAEDGCGFQSGFNEETCLVKITGLLEFEVYLEYLNRFESSEQARAVQMSTK 456
Db 149 VLIQFLOKKAKNLDAITTPDPTTNASLLTKLQAOQNWLDQMTTHILRSKEFLQSSLA 208
Qy 457 VLIQFLOKKAKNLDAITTPDPTTNASLLTKLQAOQNWLDQMTTHILRSKEFLQSSLA 516
```

```
Db 209 L 209
Qy 517 L 517

RESULT 3 PRELIMINARY; PRT; 209 AA.
ID Q28819;
AC Q28819;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
RN
RP SEQUENCE FROM N.A.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL; L46802; AAB01430.1; -.
DR HSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1 1
FT NON_TER 209 209
SQ SEQUENCE 209 AA; 23483 MW; 29B594E3 CRC32;

Query Match 21.6%; Score 814; DB 6; Length 209;
Best Local Similarity 59.2%; Pred. No. 7.29e-146;
Matches 109; Conservative 35; Mismatches 40; Indels 0; Gaps 0;

Db 26 PGPVGESQADATSNRPPLSPDRKEBFIKYILGKISALRKEMCDKYNKCEDSKAEALAE 85
Qy 337 PVPFGDSKDVAAHPHQPLTSRERIDKQIRYILDIGISALRKETCNKSNMCESSKEALAE 396
Db 86 NLRLPKLAEDGCGFQSGFNEETCLVKITGLLEFEVYLEYLNRFESSEQARAVQMSTK 145
Qy 397 NLNPKMAEDGCGFQSGFNEETCLVKITGLLEFEVYLEYLNRFESSEQARAVQMSTK 456
Db 146 LLVQMLKKYKSDQEVTPDPTTDSQAILKADQKWLKHTTHILRSLEDFLQFSLRA 205
Qy 457 VLIQFLOKKAKNLDAITTPDPTTNASLLTKLQAOQNWLDQMTTHILRSKEFLQSSLA 516
Db 206 VRIM 209
Qy 517 LRQM 520

RESULT 4 PRELIMINARY; PRT; 205 AA.
ID Q28747;
AC Q28747;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Orcinus orca (killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Orcinus.
RN
RP SEQUENCE FROM N.A.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
Southern sea otter (Enhydra lutris nereis).";
RL
```

```
RL Immunogenetics 43:190-195(1996).
DR EMBL; L46803; AAB01429.1; -.
DR HSP; P05231; 1ALU.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 205 AA; 23266 MW; C853C8DF CRC32;

Query Match
Best Local Similarity 21.5%; Score 810; DB 6; Length 205;
Matches 111; Conservative 36; Mismatches 35; Indels 1; Gaps 1;

Db 21 PGPGLGDFKDDTSDRLTSPDKTEALIKYILGKISAMRKEMCEKYDKCNSKEALAEN 80
QY 337 PVPGLGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 81 NLNPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYLNQYEGDKGAEAVQISK 140
QY 397 NLNPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYLNQYEGDKGAEAVQISK 140
Db 141 ALAQILROKVKNPDEVTTPDPTTNASLMNLOSQNDWMKNTKIILRLSLENFLQFSLR 200
QY 457 VLIQFLQKAKKALDAITTPDPTTNASLLTKLQAQNO-WLQDWTTHLLRSFKREFLOSSLR 515
Db 201 AIR 203
QY 516 ALR 518

RESULT 5
ID Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN 6 PRECURSOR.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Monodontidae;
OC Delphinapterus.
RN [1]
RP SEQUENCE FROM N.A.
RA ST-LAURENT G., DE GUISE S., FOURNIER M., ARCHAMBAULT D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AADA2929.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; OFA70646 CRC32;

Query Match
Best Local Similarity 21.3%; Score 804; DB 6; Length 208;
Matches 110; Conservative 36; Mismatches 36; Indels 1; Gaps 1;

Db 24 PGPGLGDFKDDTSDRLTSPDKTEALIKYILGKISAMRKEMCEKYDKCNSKEALAEN 83
QY 337 PVPGLGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 84 NLNPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYLNQYEGDKGAEAVQISK 143
QY 397 NLNPKMAEKDCGFCGSGFNQETCLMRITTTGLLEYQIYLDYLNQYEGDKGAEAVQISK 143
Db 144 ALAQILROKVKNPDEVTTPDPTTNASLMNLOSQNDWMKNTKIILRLSLENFLQFSLR 203
QY 457 VLIQFLQKAKKALDAITTPDPTTNASLLTKLQAQNO-WLQDWTTHLLRSFKREFLOSSLR 515
Db 204 AVR 206
QY 516 ALR 518

RESULT 6
ID O97535 PRELIMINARY; PRT; 160 AA.
AC O97535;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
RN [1]
RP SEQUENCE FROM N.A.
RA ECHEVERRY S.J., HERNANDEZ E., MORENO A., PATARROYO M.E., MURILLO L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
RT in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014505; AAD01531.1; -.
DR HSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 160 AA; 17855 MW; EF6090C3 CRC32;

Query Match
Best Local Similarity 19.8%; Score 748; DB 6; Length 160;
Matches 105; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 29 PVPGLGDSKEVAAPNRQLLTSTEQIDKHRYILEGIAALRKEICDKSNMCCSKEALAEN 88
QY 337 PVPGLGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 89 NLNPKMAEKDCGFCGSGFNQETCLMTTGLLEFVYLYLQNRFFESSEQARAVQMSK 148
QY 397 NLNPKMAEKDCGFCGSGFNQETCLMTTGLLEFVYLYLQNRFFESSEQARAVQMSK 148
RESULT 7
ID Q28403 PRELIMINARY; PRT; 207 AA.
AC Q28403;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Enhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Mustelidae; Enhydra.
RN [1]
RP SEQUENCE FROM N.A.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,
RA STOTT J.L., FERRICK D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL; L46804; AAB01428.1; -.
DR HSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 207 AA; 23527 MW; OF2CACG2 CRC32;

Query Match
Best Local Similarity 19.2%; Score 725; DB 6; Length 207;
Matches 100; Conservative 42; Mismatches 40; Indels 2; Gaps 2;

Db 26 PGPGLGDSKDDATSNRPLTSDKMDFTKFIILGKISALRNEMCDKYNKCEDSKEVLAEN 85
QY 337 PVPGLGDSKDVAAAPHRQPLTSSERIDKQIRYILDGTSALRKETCNKSNMCCSKEALAEN 396
Db 86 NLNPKMAEKDCGFCGSGFNQETCLMTTGLLEFVYLYLQNRFFESSEQARAVQMSK 145
QY 397 NLNPKMAEKDCGFCGSGFNQETCLMTTGLLEFVYLYLQNRFFESSEQARAVQMSK 145
```

```

Db 146 HLLQTLRPM-NOIE-VTPDPDTTASLQALFKSQDKWLKHTTIHLIRLLEDFLOFSURA 203
QY 457 VLIQFLOKAKNLDAITPDTTASLTKLQAQONQWLQDMTHLILRSFKFLQSSURA 516
Db 204 IRIM 207
QY 517 LRQM 520

RESULT 8
ID Q9WVQ8 PRELIMINARY; PRT; 210 AA.
AC Q9WVQ8;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE IL-6 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA NISHIDA E.;
RT "APA hamsters IL-6 partial cDNA.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028635; BAA78766.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 210 AA; 24060 MW; 0307F113 CRC32;

Query Match 14.3%; Score 539; DB 11; Length 210;
Best Local Similarity 38.8%; Pred. No. 2.71e-85;
Matches 71; Conservative 51; Mismatches 59; Indels 2; Gaps 2;

Db 28 VRRGDETD-TTPNRPVYTTQQVGGVTVVYREIYELRKLCCNNPCCMDNDVLLENN 86
QY 338 VPPGDSKDVAAPIHQPIUTSERIDKQIRYILDGISAURKCTCNKSNWCESSKALAE 397
Db 87 LELPVIQINDCLOTGYNWEICLKITSGLDYQIYLEFVNNVQDNKKDKARVIOSTIK 146
QY 398 LNLPKMAEKDCFGSGNEETCLVKIITGLLEFVLEYLQNR-ESSEQARAVQSTK 456
Db 147 TLSQIFQEVKGPDKIYTPSPSTKAILMEKLESQKWPRTKILIKALEEFLEVTVMS 206
QY 457 VLIQFLOKAKNLDAITPDTTASLTKLQAQONQWLQDMTHLILRSFKFLQSSURA 516
Db 207 TRQ 209
QY 517 LRQ 519

RESULT 9
ID Q88507 PRELIMINARY; PRT; 372 AA.
AC Q88507;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR.
GN CNTR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, SKELETAL MUSCLE;
RA MAEDA M., YAGUCHI N., HANYUU C., NAKATA Y., ONODA N., TULIN E.E.,
RA KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
RT "Mouse homolog of human ciliary neurotrophic factor receptor.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068615; AAC25711.1; -.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; ig; 1.
SQ Signal.

```

```

FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; 9A40FE12 CRC32;

Query Match 11.0%; Score 415; DB 11; Length 372;
Best Local Similarity 30.8%; Pred. No. 7.68e-59;
Matches 105; Conservative 81; Mismatches 131; Indels 24; Gaps 21;

Db 11 AVLAATAAAYTKHQSPQEAHVQYERL-GADVTLPC-GTASWD-AAVTW--RVNGTDLA 65
QY 11 ALLAAPGAALAPRRCPAQEAVARGVLTSLPGDSVTLTCTGVEPEDNATVHWLRLKPAAGSH 70
Db 66 PDLLG-SQ-LILRSLEIGHSGSLVACHRDSWHLRHQVLLHVGPPRPVPLSC-RSNTYP 122
QY 71 PSRWAGMGRULLSLVQLHDSGNSCY-RAGRAGTGVHLL-VDVPPPEQLSCFRKSPLS 128
Db 123 KGYCSW-HLPTTYIPNT-FNVTVLHGS---KIMV-CE-KDPALKNRCHRYMHLFSTI 175
QY 129 NVV-CWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAVPEGDSF 187
Db 176 KYKVISVSNALGNH-TTATFDEFTIVKPPDENVARVPVSNRRLEVWQTPSTWPD 234
QY 188 -YIVSMCVASSVSGSKFSTQTQFGGILQDPDPANITVTAVARNPRLSVTWQDPHWS-N 245
Db 235 PESPLKFFELRYRLIILDQWHLVSDGTAH-TITDAVAGKEYIIQVAAKDN-EIGTWS 292
QY 246 SSFYELRFEFLRYRAERSKFTFTTWVKDLOHCVIHDWSGLRHVVQLRAEEFGQGE 305
Db 293 WSAHAHATPMTPEPRHLTTEAQAPETTTSTSSLAPPTTK 333
QY 306 WSPEAMGTPMTE-SRSPARGGGGGGSGVPEVPVPGEDSK 345

RESULT 10
ID Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAI OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE; 95045367.
RA HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M.,
RA GOUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.;
RT "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
RT for high affinity binding and signal transduction.";
RL EMBO J. 13:4765-4775(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA NEUHAUS H., BETTENHAUSEN B., BILINSKI P., SIMON-CHAZOTTES D.,
RA GUENET J.L., GOSSLER A.;
RL Dev. Biol. 166:521-542(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6;
RA GOSSLER A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K., GOSSLER A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RT mouse genome.";
RL Biochem. J. 320:359-363(1996).

```

CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. BINDS TO IL-11
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X74953; CAA52908.1; -
 DR EMBL: U14412; AAS33248.1; -
 DR EMBL: X94162; CAA63873.1; -
 DR EMBL: X94163; CAA63873.1; JOINED.
 DR HSSP: P16471; 1BP3.
 DR MGD; MGI:107426; I111ral.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; ig; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 FT CONFLICT 384 384
 SQ SEQUENCE 432 AA; 46655 MW; F65B3060 CRC32;
 Query Match 10.88; Score 406; DB 11; Length 432;
 Best Local Similarity 30.38; Pred. No. 5.91e-57;
 Matches 110; Conservative 79; Mismatches 155; Indels 19; Gaps 18;
 Db 1 MSSSCSGLTRVLVAVATALLVSSSPCPQAWGPPGVQGPGRVMLCCPGV-SAG-TPVS 58
 QY 2 LAVGCCALLAALAAAGALAPRCP-AQE-VARGVLTSLPGDSVTLTCGVEPEDNATVH 59
 Db 59 W-FRDGDSRLQGPDSGLGHLRLVLAQVDSDEGTYYVCOITLDGVSGGMVTLKLGFPARPE 117
 QY 60 WVLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNYSCYR-AGRPACTVHLLVDVPEEPQ 118
 Db 118 VSC-QAVDYENFSCWSPQVSGLPTRYLTSYRK-KTLPGAESQRESPTSGMPWCPQDPL 175
 QY 119 LSCFRKSPLSNVVCEWGPSTSLTTKAVLLVRKFQNSPAEDFQ-EPCQYSQ-E-SQK-F 174
 Db 176 EASRCVVHGAEFSEYRINVTENPLGASTCLLDVRLQ-SILRPPDPQGLRVESVPGYPR 234
 QY 175 -SCQLAVPEGD-SSFYIVSMCVASSVGSKFTQTFQGGILQDPDPANITVAVARNR 232
 Db 235 RLHASTYTPASRRORPHFLKFLRYRPAQHPAMSTVEPIGLEE--VITDAVAGLPHAYR 292
 QY 233 WLSVTWQDPHSWNS-SFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWSGLRHVVQ 291
 Db 293 VSADEFLDAGTWSANSPAWGTPSTGPL-QDEIPDWSQGHQQLAVVAQEDSPAPRPS 351
 QY 292 LRAQEEFGQGEWSPEAMGTPWTESRPPARGGGGGGGGVPEVPPEGDSKDVAAAPH 351
 Db 352 LQP 354
 QY 352 RQP 354
 RESULT 11
 ID P70225 PRELIMINARY; PRT; 432 AA.
 AC P70225; 009074;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
 DE (IL-11BETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
 GN IL11RA2 OR IL-11BETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CD1; TISSUE=TESTIS;
 RX MEDLINE; 97129000.
 RA BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K., GOSSLER A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the
 RT mouse genome.";
 RL Biochem. J. 320:359-363(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=TESTIS;
 RX MEDLINE; 96278810.
 RA ROBB L., HILTON D.J., WILLSON T.A., BEGLEY C.G.;
 RT "Structural analysis of the gene encoding the murine interleukin-11
 RT receptor alpha-chain and a related locus.";
 RL J. Biol. Chem. 271:13754-13761(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=TESTIS;
 RX MEDLINE; 97230451.
 RA ROBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;
 RT "Identification of a second murine interleukin-11 receptor alpha-chain
 RT gene (IL11ra2) with a restricted pattern of expression.";
 RL Genomics 40:387-394(1997).
 CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE IG-LIKE DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 DR EMBL: X94157; CAA63872.1; -
 DR EMBL: X94158; CAA63872.1; JOINED.
 DR EMBL: X94159; CAA63872.1; JOINED.
 DR EMBL: X94160; CAA63872.1; JOINED.
 DR EMBL: X94161; CAA63872.1; JOINED.
 DR EMBL: X98519; CAA67144.1; -
 DR EMBL: U69491; AAC53114.1; -
 DR HSSP: P16471; 1BP3.
 DR MGD; MGI:109123; I111ra2.
 DR PFAM; PF00041; fn3; 2.
 DR PFAM; PF00047; ig; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 432
 FT DOMAIN 24 367
 FT TRANSMEM 368 393
 FT DOMAIN 394 432
 FT DOMAIN 41 102
 FT CARBOHYD 127 127
 FT CARBOHYD 194 194
 FT CONFLICT 200 200
 FT CONFLICT 384 384
 SQ SEQUENCE 432 AA; 46721 MW; C4FD7DEC CRC32;
 Query Match 10.68; Score 401; DB 11; Length 432;
 Best Local Similarity 30.38; Pred. No. 6.57e-56;
 Matches 110; Conservative 79; Mismatches 155; Indels 19; Gaps 18;
 Db 1 MSSSCSGLTRVLVAVATALLVSSSPCPQAWGPPGVQGPGRVMLCCPGV-SAG-TPVS 58
 QY 2 LAVGCCALLAALAAAGALAPRCP-AQE-VARGVLTSLPGDSVTLTCGVEPEDNATVH 59
 Db 59 W-FRDGDSRLQGPDSGLGHLRLVLAQVDSDEGTYYVCOITLDGVSGGMVTLKLGFPARPE 117
 QY 60 WVLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNYSCYR-AGRPACTVHLLVDVPEEPQ 118
 Db 118 VSC-QAVDYENFSCWSPQVSGLPTRYLTSYRK-KTLPGAESQRESPTSGMPWCPQDPL 175
 QY 119 LSCFRKSPLSNVVCEWGPSTSLTTKAVLLVRKFQNSPAEDFQ-EPCQYSQ-E-SQK-F 174
 Db 176 EASRCVVHGAEFSEYRINVTENPLGASTCLLDVRLQ-SILRPPDPQGLRVESVPGYPR 234
 QY 175 -SCQLAVPEGD-SSFYIVSMCVASSVGSKFTQTFQGGILQDPDPANITVAVARNR 232

Db 61 LOSQEWLHRTHTLRLKLEDFLOFSLRVRIM 94
 QY 487 LOAQONWLODMTTHILRSFKFLOSSLRALRQM 520

RESULT 15
 ID O55041 PRELIMINARY; PRT; 101 AA.
 AC O55041;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HEINE H., DELODE R.D., MONKS B., GOLENBOCK D.T.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF044667; AAC02100.1; -.
 DR HSSP; P05231; 2IL6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR PFW; PF00489; IL-6; 1.
 DR NON_TER 1
 FT NON_TER 101
 SQ SEQUENCE 101 AA; 11749 MW; DIDA362A CRC32;

Query Match 8.7%; Score 329; DB 11; Length 101;
 Best Local Similarity 41.2%; Pred. No. 4.52e-41;
 Matches 40; Conservative 28; Mismatches 28; Indels 1; Gaps 1;

Db 5 NDGCYOTGYNWEICLLKITSGLDYIYLFVTNNVQDNKKDKARVIOSTTKTLQIIFKQ 64
 QY 406 KDCCFQSGFNEETCLVKITGLLEFEVILEYIQNRF-ESSEQARAVQMSTKVLIOFLQK 464

Db 65 EVKDPDKIVMPSPSKAILIEKLESQKOMPRTKTIEL 101
 QY 465 KAKNLDAITTPDPTTNASLLTKLQACNOWNLODMTTHL 501

Search completed: Thu Aug 10 16:19:18 2000
 Job time : 151 secs.

This Page Blank (uspio)

MASSRCH_PP

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:15:35 2000; MasPar time 17.31 Seconds
Tabular output not generated. 930.844 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.ppe
Perfect Score: 3771
Sequence: 1 MLAGVCGALLAALLAAPGAAL.....LILRSFKFELQSSLRALRQ 520

Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 50.665; Variance 86.177; scale 0.588

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.6	468	1 IL6A_HUMAN	INTERLEUKIN-6 RECEPTOR	0.00e+00
2	1361	36.1	462	1 IL6A_RAT	INTERLEUKIN-6 RECEPTOR	2.44e-290
3	1320	35.0	460	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	2.98e-280
4	1287	34.1	212	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	3.84e-272
5	1257	33.3	212	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	8.91e-265
6	1251	33.2	212	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	1.34e-263
7	1244	33.0	212	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	1.34e-261
8	814	21.6	209	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	4.33e-157
9	810	21.5	205	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	3.95e-156
10	806	21.4	208	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	3.60e-155
11	801	21.2	212	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	5.69e-154
12	786	20.8	208	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	2.23e-150
13	786	20.8	208	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	2.23e-150
14	693	18.4	208	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	3.34e-128
15	683	18.1	208	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	7.87e-126
16	680	18.0	208	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	4.05e-125
17	654	17.3	207	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	5.75e-119
18	560	14.9	211	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	6.70e-97
19	558	14.8	211	1 IL6A_MOUSE	INTERLEUKIN-6 RECEPTOR	1.96e-96
20	491	13.0	125	1 IL6A_MOUSE	INTERLEUKIN-6 (IL-6) (6.39e-81
21	409	10.8	372	1 CNTR_RAT	CILIARY NEUTROTROPIC F	2.94e-62
22	408	10.8	372	1 CNTR_HUMAN	CILIARY NEUTROTROPIC F	4.93e-62
23	373	9.9	362	1 CNTR_CHICK	CILIARY NEUTROTROPIC F	3.26e-54

ALIGNMENTS

RESULT	1	IL6A_HUMAN	STANDARD;	PRT;	468 AA.
ID	IL6A_HUMAN	STANDARD;	PRT;	468 AA.	
AC	P08867;				
DT	01-NOV-1988 (Rel. 09, Created)				
DT	01-NOV-1988 (Rel. 09, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA) (CD126 ANTIGEN).				
DE	ANTIGEN).				
GN	IL6R.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 88305347.				
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,				
RA	Taniguchi T., Hirano T., Kishimoto T.;				
RT	"Cloning and expression of the human interleukin-6 (BSP-2/IFN beta 2) receptor".				
RL	Science 241:825-828(1988).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,				
RA	Taniguchi T., Hirano T., Kishimoto T.;				
RL	"Molecular structure of interleukin 6 receptor".				
RN	Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 91336983.				
RA	Schoellink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,				
RA	Kishimoto T., Heinrich P.C., Rose-John S.;				
RT	"Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells."				
RL	Biochem. J. 277:659-664(1991).				
CC	-!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.				
CC	-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.				
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.				
CC	-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.				
CC	-!- DATABASE: NAME=PROW; NOTE=CD guide CD126 entry;				
CC	-!- WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd126.htm"				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its				

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: X12830; CAA31312.1; -;
EMBL: X58298; CAA41231.1; -;
PIR: A41242; A41242.
PIR: J00080; J00080.
PIR: S14621; S14621.
PIR: S17468; S17468.
MIM: 147880; -;
PFAM: PF00041; fn3; 1.
PFAM: PF00047; ig; 1.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.

Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;

Signal.
CHAIN 1 19
DOMAIN 20 468
TRANSMEM 21 358
DOMAIN 359 386
DOMAIN 387 468
DOMAIN 40 103
DISULFID 47 96
DISULFID 121 132
DISULFID 165 176
CARBOHYD 55 55
CARBOHYD 93 93
CARBOHYD 221 221
CARBOHYD 245 245
CARBOHYD 350 350
SEQUENCE 468 AA; 51547 MW; 62AA239FA14F1B8B CRC64;

Query Match 63.6%; Score 2398; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGALLAALLAALPAGALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy 1 MLAVGALLAALLAALPAGALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDPPEEPOLS 120
Qy 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDPPEEPOLS 120
Db 121 CFRKSPNSVVCVCGPSTPSLTITKAVLLVRKFNQSPAEFQPCQYSOESQKSCQLAV 180
Qy 121 CFRKSPNSVVCVCGPSTPSLTITKAVLLVRKFNQSPAEFQPCQYSOESQKSCQLAV 180
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGIILQPPANITVAVARNRWLSVTWQD 240
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGIILQPPANITVAVARNRWLSVTWQD 240
Db 241 PHSNNSFYRLRFELRYAERSKFTTMMVKDLQHCVHIDAWSLRHVQLRAQEFGQ 300
Qy 241 PHSNNSFYRLRFELRYAERSKFTTMMVKDLQHCVHIDAWSLRHVQLRAQEFGQ 300
Db 301 GEWSNPSPAMGTPWTSRSPPA 323
Qy 301 GEWSNPSPAMGTPWTSRSPPA 323

RESULT 2
ID IL6A_RAT STANDARD; PRT; 462 AA.
AC P22273;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
GN IL6R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FISCHER 344; TISSUE=LIVER;
EX MEDLINE; 91060602.
RA Baumann M., Baumann H., Fey G.H.;
RT "Molecular cloning, characterization and functional expression of the
RL rat liver interleukin 6 receptor";
RN J. Biol. Chem. 265:19853-19862(1990).
[2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RA Gibson T.;
RL Unpublished observations (FEB-1995).
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; M58587; AAA41431.1; -;
PIR; A37986; A37986.
HSP; P16471; 1BP3.
PFAM; PF00041; fn3; 1.
PFAM; PF00047; ig; 1.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
Signal.
CHAIN 1 19
DOMAIN 20 462
TRANSMEM 21 357
DOMAIN 358 385
DOMAIN 386 462
DISULFID 47 92
DISULFID 117 128
DISULFID 162 173
CARBOHYD 32 32
CARBOHYD 85 85
CARBOHYD 150 150
CONFLICT 227 261
SEQUENCE 462 AA; 50398 MW; A4D6064CEDC0537D CRC64;
Query Match 36.1%; Score 1361; DB 1; Length 462;
Best Local Similarity 55.6%; Pred. No. 2.44e-290;
Matches 188; Conservative 58; Mismatches 85; Indels 7; Gaps 4;

Db 1 MLAVGCTLLVALLAALPAVALVGLSCRALEVANGVTVSLPGATVTLICPGKEAAGNATVHW 60
Qy 1 MLAVGCTLLVALLAALPAVALVGLSCRALEVANGVTVSLPGATVTLICPGKEAAGNATVHW 60
Db 61 VY----SGSQSREWTGNTLVRAVQVNDTGHVLCFLDHLVGTVPVLVDPPEEPKLS 116
Qy 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRAGTAVHLLVDPPEEPOLS 120
Db 117 CFRKNPLVNAFCWHPSPSTPTTKAVMFAKNTNTNGKSDFOVPCQYSOQLKSFSCVE 176
Qy 121 CFRKSPNSVVCVCGPSTPSLTITKAVLLVRKFNQSPAE--DFQEPQYSOESQKSCOLA 179
Db 177 ILBGDKVYHIVSLCVANSVSGSRSHNVVFSQSLKMWQVQPPANILVVAIPGPRWLKYSWQ 236

```

QY 180 VEGSSFYIVSMCVSSVSGSFSTQTFQGGILQDPPANITVAVARNRWLSVTWQ 239
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 237 DPESDPSYILLOFLRYRPVWKKFTTVMPLQVAOHCQVHDLRGVHVQVRCKEED 296
      || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 240 DPHSNWSFYRLRFLRYRAERSKFTTVMVKDLQHCVHIDWAGSLRHVVQLRAQEFG 299
      || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 297 IQGSKWSPEVTGTPLAEPRTTPA-GIPGNPTQVSVE 333
      || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 300 QGEWSEWSPAMGTPW-TESRPPARGGGGGGGGSVE 336
      || ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

RESULT 3
ID IL6A_MOUSE STANDARD; PRT; 460 AA.
AC P22272;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR (IL-6R-ALPHA).
GN IL6RA OR IL6R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE; 90278354.
RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytomagenesis."
RT J. Exp. Med. 171:2001-2009(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H; TISSUE=LIVER;
RA Florillo M.T., Ciliberto G., Dente L.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X51975; CAA36237.1; -.
DR EMBL; X53802; CAA37810.1; -.
DR PIR; JL0145; JL0145.
DR PIR; S14543; S14543.
DR HSP; P16471; IBP3.
DR MGD; MG1:105304; IL6RA.
DR PFAM; PF00041; fn3; 1.
DR PFAM; PF00047; 1g; 1.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW SIGNAL.
FT CHAIN 1 19 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT CHAIN 20 460
FT DOMAIN 21 357 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 358 385 POTENTIAL.
FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 47 92 POTENTIAL.

```

```

FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 POTENTIAL.
FT CARBOHYD 55 55 POTENTIAL.
FT CARBOHYD 150 150 POTENTIAL.
FT CONFLICT 374 374 A -> R (IN REF. 2).
SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 35.0%; Score 1320; DB 1; Length 460;
Best Local Similarity 55.1%; Pred. No. 2.98e-280;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;

Db 1 MLTGVCTLLVALLAAPAVALLVGLSCRALEFVANGTTSIPGATVTLICPGKEAGNVTHW 60
      |||||:|||||: || ||| : |||||: ||| ||| : |||||: ||| ||| : |||||
QY 1 MLAVGCALLAALLAAPGAALPRCPAQEVARGLVLSLPGDSVTLTCGVEPDNATVHW 60
      |||||:|||||: || ||| : |||||: ||| ||| : |||||: ||| ||| : |||||
Db 61 VY----SGSQNRWTTGNTLVLRDVQLSDTGDIYLCSLNDHLVGTVPVLVDVPPPEPKLS 116
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 61 VLRKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNSYCRAGRAGTGVHLLVDVPPPEPKLS 120
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 117 CFRKNPLVNAICEWRSPSTPTTKAVLFAKKINTNGSKDFQVPCOYSQLKSFSCOVE 176
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
QY 121 CFRKPSLNVNVCWGPSPSTPTTKAVLLVRKFQNSPAB-DFQEPQCYSQESQKESCQLA 179
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 177 ILEGDKVYHIVSLCVANSYSGSSSHNEAFHSLKMQVQPPDPANLVSAIPGRPRWLKVSQ 236
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 180 VEGDSSFYIVSMCVSSVSGSFSTQTFQGGILQDPPANITVAVARNRWLSVTWQ 239
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 237 HPETWDPYSYLLQFLRYRPVWKKFTTVMPLQVAOHCQVHDLRGVHVQVRCKEED 296
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
QY 240 DPHSNWSFYRLRFLRYRAERSKFTTVMVKDLQHCVHIDWAGSLRHVVQLRAQEFG 299
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 297 LGQWSEWSPAMGTPW-TESRPPA 321
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
QY 300 QGEWSEWSPAMGTPW-TESRPPA 323
      |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||

RESULT 4
ID IL6_HUMAN STANDARD; PRT; 212 AA.
AC P05231.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
DE (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).
DE IL6 OR IFNB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE; 87065033.
RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
RA Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
RT B lymphocytes to produce immunoglobulin.";
RT Nature 324:73-76(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88082664.
RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
RA Nakai S., Kishimoto T.;
RT "Structure and expression of human B cell stimulatory factor-2
RT (BSF-2/IL-6) gene.";
RL EMBO J. 6:2939-2945(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87067433.
RA May L.T., Helgott D.C., Sehgal P.B.;
RT "Anti-beta-interferon antibodies inhibit the increased expression of
RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
RT structural studies of the beta 2 interferon involved.";

```

Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 [4] SEQUENCE FROM N.A.
 RN MEDLINE; 87053818.
 RX Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
 RA "Structure and expression of cDNA and genes for human
 RT interferon-beta-2, a distinct species inducible by growth-stimulatory
 RT cytokines.";
 RL EMBL J. 5:2529-2537(1986).
 RN [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 88088768.
 RX Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 RA Aarden L.A.;
 RA "Molecular cloning and expression of hybridoma growth factor in
 RT Escherichia coli.";
 RL J. Immunol. 139:4116-4121(1987).
 RN [6]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 89391958.
 RX Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
 RA "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [7]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 89193317.
 RX Wong G., Wittek-Giannotti J., Hewick R., Clark S., Ogawa M.;
 RA "Interleukin 6: identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [9]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 93178270.
 RX Chen Q.Y.;
 RA "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [10]
 RN SEQUENCE OF 30-63.
 RX MEDLINE; 88154445.
 RX van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.;
 RA "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RN SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE; 95154344.
 RX Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
 RA Zilio R., de Filippis V., Polverino de Laureto P., Fontana A.;
 RA "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RN DISULFIDE BONDS.
 RX MEDLINE; 89286115.
 RX Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
 RA "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).

RN [13] MUTAGENESIS.
 RP MEDLINE; 91243808.
 RX Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
 RA "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RN STRUCTURE BY NMR.
 RX MEDLINE; 96134845.
 RX Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RA "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RN STRUCTURE BY NMR.
 RX MEDLINE; 97303053.
 RX Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA Cumming D.A.;
 RA "Solution structure of recombinant human interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE; 97224126.
 RX Somers W., Stahl M., Seehra J.S.;
 RA "1.9-A crystal structure of interleukin 6: implications for a novel
 RT mode of receptor dimerization and signaling.";
 RL EMBL J. 16:989-997(1997).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X04430; CAA28026.1; -
 CC EMBL; M14584; AAA52728.1; -
 CC EMBL; X04602; CAA28268.1; -
 CC EMBL; Y00081; CAA68278.1; -
 CC EMBL; M18403; AAA52729.1; -
 CC EMBL; M29150; AAA59154.1; -
 CC EMBL; X04402; CAA27990.1; -
 CC EMBL; X04403; CAA27991.1; -
 CC EMBL; M54894; AAC41704.1; -
 CC EMBL; M56892; AAD13886.1; -
 CC EMBL; A09363; CAA00839.1; -
 CC PIR; A32648; IVHUB2.
 CC PIR; A25921; A25921.
 CC PDB; 1IL6; 04-FEB-98.
 CC PDB; 2IL6; 04-FEB-98.
 CC PDB; 1ALU; 03-JUN-98.
 CC MIM; 147620; -
 CC PFAM; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSFPMGF.
 CC PRINTS; PR00434; INTERLEUKIN6.
 CC PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 73 73
 FT MUTAGEN 173 173
 FT MUTAGEN 185 185
 FT A->V: ALMOST NO LOSS OF ACTIVITY.
 FT W->R: NO LOSS OF ACTIVITY.

FT MUTAGEN 204 204 S->P: 13% ACTIVITY.
 FT MUTAGEN 210 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
 FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
 SQ SEQUENCE 212 AA; 23718 MW; 1FIEDIFE1B734079 CRC64;

Query Match 34.1%; Score 1287; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 3.84e-272;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 PVPVGGDSKDVAAAPHROPLTSSERIDKQIRYILDGTSALRKETCNKNMCSKEALAEN 88
 |||||||
 QY 337 PVPVGGDSKDVAAAPHROPLTSSERIDKQIRYILDGTSALRKETCNKNMCSKEALAEN 396
 |||||||

Db 89 NNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 148
 |||||||
 QY 397 NNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 456
 |||||||

Db 149 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQANQOWLQDMTHLILRSKFQSSLR 208
 |||||||
 QY 457 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQANQOWLQDMTHLILRSKFQSSLR 516
 |||||||

Db 209 LRQM 212
 |||||

QY 517 LRQM 520
 |||||

RESULT 5
 ID IL6_MACFA STANDARD; PRT; 212 AA.
 AC P79341;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tatsumi M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB000554; BAA19148.1; -
 DR HSSP; P05231; 2116.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PROSITE; PR00434; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT DISULFID 101 111 POTENTIAL.
 FT CARBOHYD 73 73 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

Query Match 33.3%; Score 1257; DB 1; Length 212;

Best Local Similarity 96.7%; Pred. No. 8.91e-265;
 Matches 178; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 29 PVLPGEDSKDVAAAPHROPLTSSERIDKHRYILDGTSALRKETCNRSNMCESKEALAEN 88
 |||||||
 QY 337 PVLPGEDSKDVAAAPHROPLTSSERIDKHRYILDGTSALRKETCNRSNMCESKEALAEN 396
 |||||||

Db 89 NNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 148
 |||||||
 QY 397 NNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEEQARAVQMSK 456
 |||||||

Db 149 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQANQOWLQDMTHLILRSKFQSSLR 208
 |||||||
 QY 457 VLIQFLOKAKKALDAITTPDPTTNASLLTKLQANQOWLQDMTHLILRSKFQSSLR 516
 |||||||

Db 209 LRQM 212
 |||||

QY 517 LRQM 520
 |||||

RESULT 6
 ID IL6_MACMU STANDARD; PRT; 212 AA.
 AC P51494;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RAC 2;
 RX MEDLINE; 960003435.
 RA Villinger F.J.; Brar S.S.; Mayne A.E.; Chikkala N.; Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 RT nonhuman primates";
 RL J. Immunol. 155:3946-3954(1995).
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L26028; AAA99978.1; -
 DR HSSP; P05231; 1ALU.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PROSITE; PR00434; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT DISULFID 101 111 POTENTIAL.
 FT CARBOHYD 73 73 POTENTIAL.
 FT CARBOHYD 172 172 POTENTIAL.
 SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCCAD CRC64;

Query Match 33.2%; Score 1251; DB 1; Length 212;
 Best Local Similarity 95.7%; Pred. No. 2.64e-263;
 Matches 176; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

	Query Match	21.2%	Score 801;	DB 1;	Length 212;
	Best Local Similarity	59.9%	Pred. No.	5.69e-154;	
	Matches	107;	Conservative	37;	Mismatches 35; Indels 0; Gaps 0;
D b	34	EDAKGATSDKMLFTSPDKTEELIKYILGKISAMRCEMCKEYKEPCNSKEVLAENNLNP	93	: :: ::: :: :	: : : :
Q y	342	EDSKDVAAPHRQPITTSERIDKOIRYLGISALRKETCNKNCSSEKAELAENNLNP	401	:	: :
D b	94	KMAEKDCFCQSGFNQBCTCLMRITTGLVEFYLDYLOKEYESNKGWNEAVQISTRALIQT	153	: : : : : : : : : : : : : : :	
Q y	402	KMAEKDCFCQSGFNETCIVKWIIITLLEFEVYLEYLNRFESSEEQAQAVQMSTKVLIQF	461	:	:
D b	154	LROQGNPKOKATTPNPTTNAGLLDLKLQSONEWMKNTKIILIRSLBEDTFQLFSURATRIM	212	: :	:
Q y	462	LORKKANLDIAITPDPTTNASLTTLKQANONIQDMTHIILIRSFEEFLQSSLRALROM	520	: :	:

```

RESULT 12
ID IL6_CANFA STANDARD; PRT; 207 AA.
AC P41323;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
[1]
SEQUENCE FROM N.A.
RC STRAIN-MONGREL;
RX MEDLINE; 94303924.
RA Kukielka G.L., Youker K.A., Hawkins H.K., Perrard J.L.,
RA Michael L.H., Ballantyne C.M., Smith C.W., Entman M.L.;
RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
RT reperfusion.";
RT Ann. N.Y. Acad. Sci. 723:258-270(1994).
RL -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U12234; AAA83030.1; -
CC DR HSP; P05231; 21L6
CC DR PFAM; PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSXPMGF.
CC DR PRINTS; PR00434; INTERLEUKIN6.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 ? POTENTIAL.
CC CHAIN ? 207 INTERLEUKIN-6.
CC FT DISULFID 67 73 BY SIMILARITY.
CC FT DISULFID 96 106 BY SIMILARITY.
CC SEQUENCE 207 AA; 22945 MW; 45540154EA9C0F50 CRC64;
CC -----
Query Match 20.8%; Score 786; DB 1; Length 207;
Best Local Similarity 58.2%; Pred. No. 2,23e-150;
Matches 107; Conservative 37; Mismatches 40; Indels 0; Gaps 0;

Ddb 24 PGPLAGSDKDDATSNLSPLTSSANKVEELIKYTLGKISALRKEMCKDFNKCDKSKALAEEN 83
| : | | | | : : : | | | | | : : | | | | | : | | | | | | | | | |
Ov 337 PYPVPGDSDKDAAPHPROTTSSTIRIDKQRYILDGTSALRKETCNKSNMCKSSKEALAEEN 396

```



```

Db 84 NLHLPKLEKDGCGFQSGFNOETCLTRITTTGLVFEHLNLQNNYEGDKENKSVHMSTK 143
QY 397 NLNLPRMAEKDGCFCGFGNEETCLVRIITGLLEFEVLEYLQNRFSSEEQARAVQMSTK 456
Db 144 ILVQMLKSVKKNODEVTTDPDPTDASLQAILQSQDECVKHTTHLLRLSLEDFLQPSLRA 203
QY 457 VLIQFLQKAKNLDIAITTPDPTTNASLLTKLQAOQWLODMTHLLRSFKPELQSSLRA 516
Db 204 VRIM 207
QY 517 LRQM 520

RESULT 13
ID IL6_FELCA STANDARD; PRT; 208 AA.
AC P41683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94162386.
RA Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
RA Hasagawa A.;
RT "Molecular cloning of feline Interleukin-6 cDNA.";
RL J. Vet. Med. Sci. 55:941-944(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOCYTES;
RX MEDLINE; 94052249.
RA Bradley W.G., Gibbs C., Kraus L., Kraus R.A., Day N.K.;
RT "Molecular cloning and characterization of a cDNA encoding feline interleukin-6.";
RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L16914; AAA16620.1; -
CC DR EMBL; D13227; BAA02507.1; -
CC DR HSP; P05231; 2IL6.
CC DR PFAM; PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFWMGF.
CC DR PROSITE; PS00434; INTERLEUKIN_6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 27 POTENTIAL.
CC FT CHAIN 28 208 INTERLEUKIN-6.
CC FT DISULFID 68 74 BY SIMILARITY.
CC FT DISULFID 97 107 BY SIMILARITY.
CC FT CONFLICT 2 2 T -> N (IN REF. 2).
CC FT CONFLICT 45 45 S -> P (IN REF. 2).
CC FT CONFLICT 133 133 E -> K (IN REF. 2).
CC FT CONFLICT 173 167 AKLSQEEWLRHTTI -> LSCSHRVAAHNN (IN REF. 2).
CC FT CONFLICT 200 201 FS -> LR (IN REF. 2).
CC FT SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

```

```

Query Match 20.8%; Score 786; DB 1; Length 208;
Best Local Similarity 57.8%; Pred. No. 2.23e-150;
Matches 100; Conservative 40; Mismatches 33; Indels 0; Gaps 0;

Db 36 ATNRLPLTSADKMEELIKYILKISALKKEMCDNYKCEDSKALAEENLNLPKLAEKD 95
QY 348 AAPHPRLDTSERIDKQIRYILDIGISALRKETCNKSNKSSCKEALAEENLNLPKMAEKD 407
Db 96 GCFQSGFNOETCLTRITTTGLQEQIYLFLODKYEGDEENAKSVYVTSNVLQMLKPKGK 155
QY 408 GCFQSGFNEETCLVKIITGLLEFEVLEYLQNRFSSEEQARAVQMSTKVLIIQFLQKRAK 467
Db 156 NODEVTIPVTEVGLQAKLSQSEWLRHTTHLTLRLRLEDFLQFSLRVAVRM 208
QY 468 NLDAITPDPTTNASLLTKLQAOQWLODMTHLLRSFKPELQSSLRALRQM 520

RESULT 14
ID IL6_BOVIN STANDARD; PRT; 208 AA.
AC P26892;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN;
RX MEDLINE; 93076003.
RA Droogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
RT "Nucleotide sequence of bovine interleukin-6 cDNA.";
RL DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X57317; CAA40572.1; -
CC DR PIR; S22162; S22162.
CC DR HSP; P05231; 2IL6.
CC DR PFAM; PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFWMGF.
CC DR PROSITE; PS00434; INTERLEUKIN_6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC FT CHAIN 30 208 INTERLEUKIN-6.
CC FT DISULFID 72 78 BY SIMILARITY.
CC FT DISULFID 101 111 BY SIMILARITY.
CC FT CARBOHYD 38 38 POTENTIAL.
CC SQ SEQUENCE 208 AA; 23758 MW; A0F000B9BA2EC341 CRC64;

Query Match 18.4%; Score 693; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 3.34e-128;
Matches 93; Conservative 46; Mismatches 39; Indels 4; Gaps 2;

Db 29 PGPIGEDFKNDTTPGRLLLTTPKEKTEALIKRMVDKISAMRKEICEKNDCESSKETLAEN 88

```

```
QY 337 PVPFGEDSKDVAAHPHQPTTSSRIDKQIRYILDGISAIRKTCNKSNMCSSKEALAEN 396
Db 89 KMLPKMEKDCGFCGQFNOACILRTTAGLLEYOIYLDLQNEVEGNOENVDRLRKNIR 148
QY 397 NLNPKMAEKDCGFCGQFNEETCLVKIITGLLEFVYLYLQNRFSSEEQARAVOMSTK 456
Db 149 TLIQILKQKIADL--ITTP--ATNTDMLKMOSSNEWKNKAVIIILRSLENFLQFSIRA 204
QY 457 VLIQFLQKKAKNLDATITPDPTTNASLLTKLQAQNWQLQDMTHLILRSFKFLQSSIRA 516
Db 205 IR 206
QY 517 LR 518
```

```
RESULT 15
ID IL6.CAPHI STANDARD; PRT; 208 AA.
AC Q28319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97392354.
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells."
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D86569; BAA13118.1; -.
CC HSPF; P05231; 2116.
CC PFAM; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN6.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC Cytokine; Glycoprotein; Growth factor; Signal.
CC SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 30 208 INTERLEUKIN-6.
CC DISULFID 72 78 BY SIMILARITY.
CC DISULFID 101 111 BY SIMILARITY.
CC CARBOHYD 38 38 POTENTIAL.
CC SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;
```

```
Query Match 18.1%; Score 683; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 7.87e-126;
Matches 93; Conservative 43; Mismatches 42; Indels 4; Gaps 2;

Db 29 PGPLGEDFKNDTTPSRLLITTPKTEALIKHIYDKISAIRKEICEKNDCEKSKETLAEN 88
QY 337 PVPFGEDSKDVAAHPHQPTTSSRIDKQIRYILDGISAIRKTCNKSNMCSSKEALAEN 396
Db 89 KMLPKMEKDCGFCGQFNOACILRTTAGLLEYOIYLDLQNEVEGNOENVDRLRKNIR 148
```

```
QY 397 NLNPKMAEKDCGFCGQFNEETCLVKIITGLLEFVYLYLQNRFSSEEQARAVOMSTK 456
Db 149 TLIQILKQKIADL--ITTP--ATNTDMLKMOSSNEWKNKAVIIILRSLENFLQFSIRA 204
QY 457 VLIQFLQKKAKNLDATITPDPTTNASLLTKLQAQNWQLQDMTHLILRSFKFLQSSIRA 516
Db 205 IR 206
QY 517 LR 518
```

Search completed: Thu Aug 10 16:16:28 2000
Job time : 53 secs.

MAISREH
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:13:42 2000; MasPar time 26.82 Seconds
Tabular output not generated. 914.465 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.pep
Perfect Score: 3771
Sequence: 1 MIAVGCALLAALLAAGPAAAL.....LILSPKFEQLQSSLRALRQM 520

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir64
1:pir1 2:pir2-3:pir3 4:pir4

Statistics: Mean 49.906; Variance 97.591; scale 0.511

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	2398	63.6	468	1	A41242	interleukin-6 recepto	0.00e+00
2	1320	35.0	440	2	JL0144	interleukin-6 recepto	7.38e-244
3	1320	35.0	460	2	JL0145	interleukin-6 recepto	7.38e-244
4	1287	34.1	212	1	IVH0B2	interleukin-6 precurs	8.47e-237
5	1095	29.0	462	1	A37986	interleukin-6 recepto	7.11e-196
6	806	21.4	208	2	T09216	interleukin-6 precurs	6.02e-135
7	801	21.2	212	2	I46590	interleukin 6 - pig	6.67e-134
8	801	21.2	212	2	I46621	prointerleukin 6 - pi	6.67e-134
9	693	18.4	208	1	A56610	interleukin-6 precurs	1.87e-111
10	680	18.0	207	2	I46084	interleukin 6 - cat	9.08e-109
11	679	18.0	208	1	S29549	interleukin-6 - sheep	1.46e-108
12	560	14.9	211	1	ICWS6	interleukin-6 precurs	3.53e-84
13	558	14.8	211	2	A34247	interleukin-6 precurs	9.01e-84
14	409	10.8	372	2	I58141	ciliary neurotrophic	5.66e-54
15	408	10.8	372	1	UHHUCN	ciliary neurotrophic	8.89e-54
16	406	10.8	432	2	I48343	interleukin-11 recept	2.19e-53
17	397	10.5	422	2	I78991	interleukin-11 recept	1.27e-51
18	373	9.9	362	2	S60614	growth promoting acti	5.92e-47
19	212	5.6	831	2	JQ1655	prolactin receptor pr	3.65e-17
20	179	4.7	201	2	A42247	myelomonocytic growth	1.30e-11
21	179	4.7	581	2	I45971	prolactin receptor -	1.30e-11
22	172	4.6	830	2	I50455	prolactin receptor -	1.77e-10
23	165	4.4	630	2	I51086	prolactin receptor -	2.33e-09

ALIGNMENTS

```
1
RESULT 1
ENTRY A41242 #type complete
TITLE Interleukin-6 receptor precursor - human
CONTAINS Interleukin-6 receptor, soluble form
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change
22-Jun-1999

ACCESSIONS A41242; J00080; S17468; A61459; S14621
REFERENCE A41242
#authors Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T.
#journal Science (1988) 241:825-828
#title Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
#cross-references MIM:88305347
#accession A41242
#molecule_type mRNA
#residues 1-468 #label YAM
#cross-references GB:M20566; NID:g186346; PID:g307062
REFERENCE J00080
#authors Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.; Hirano, T.; Kishimoto, T.
#journal Proc. Jpn. Acad. (1988) 64:209-211
#title Molecular structure of interleukin 6 receptor.
#accession J00080
#molecule_type mRNA
#residues 1-468 #label YA2
REFERENCE S17468
#authors Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, P.C.; Rose-John, S.
#journal Biochem. J. (1991) 277:659-664
#title Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells.
#cross-references MIM:91336983
#accession S17468
#molecule_type mRNA
#residues 1-468 #label SCH
#cross-references EMBL:X56298; NID:g32580; PIDN:CAA1231.1; PID:g32581
#experimental_source Hepatoma cell line HepG2
REFERENCE A61459
#authors Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
#journal J. Exp. Med. (1989) 170:1409-1414
#title Soluble cytokine receptors are present in normal human urine.
#cross-references MIM:90010793
#accession A61459
#molecule_type protein
```

```
24 155 4.1 917 2 I49699 glycoprotein 130 - mo
25 152 4.0 616 2 A30304 prolactin receptor 2
26 142 3.8 206 2 A57018 prolactin receptor -
27 144 3.8 622 2 A40144 prolactin receptor lo
28 138 3.7 265 2 S14081 erythropoietin recept
29 140 3.7 310 2 A29884 prolactin receptor pr
30 140 3.7 412 2 A41070 prolactin receptor Nb
31 140 3.7 610 2 A36116 prolactin receptor 2
32 140 3.7 918 2 A34631 lactogen receptor 1 -
33 141 3.7 610 2 A36337 membrane glycoprotein
34 139 3.7 918 2 A44257 interleukin-6 signal
35 137 3.6 292 2 I77525 prolactin receptor pr
36 137 3.6 303 2 I77524 prolactin receptor pr
37 137 3.6 608 2 I53269 prolactin receptor, 1
38 128 3.4 266 2 S61522 LMO protein - fruit f
39 127 3.4 328 2 A38957 interleukin 12b precu
40 129 3.4 805 2 JC4897 leptin receptor, Ob-R
41 129 3.4 894 2 JC4797 leptin receptor precu
42 129 3.4 895 2 S74225 leptin receptor, isof
43 129 3.4 1162 2 PC4184 leptin receptor, Ob-R
44 124 3.3 894 2 S68437 leptin receptor (vari
45 124 3.3 900 2 S68440 leptin receptor (vari
```

```
8.60e-08
2.49e-07
8.05e-06
4.05e-06
3.13e-05
1.59e-05
1.59e-05
1.59e-05
1.13e-05
2.24e-05
4.39e-05
4.39e-05
4.39e-05
1.8e-03
6.20e-04
6.20e-04
3.10e-03
```

```

##residues      20-49 ##label NOV
COMMENT      Through this receptor, interleukin-6 induces proliferation,
              activation, and differentiation of various cell types.
COMMENT      This growth factor receptor does not have a tyrosine kinase domain.
GENETICS
#gene      GDB:IL6R
#map_position      1q21-lq21
#cross-references      GDB:127966; OMIM:147880
CLASSIFICATION      #superfamily ciliary neurotrophic factor receptor; cytokine
                      receptor homology; immunoglobulin homology
KEYWORDS      acute phase; cytokine receptor; glycoprotein; transmembrane
                      protein
FEATURE
1-19      #domain signal sequence #status predicted #label SIG\
20-468      #product interleukin-6 receptor #status predicted #label
              MAT\
20-363      #domain extracellular #status predicted #label EXT\
40-98      #domain immunoglobulin homology #label IMM2\
121-309      #domain cytokine receptor homology #label CRS\
364-386      #domain transmembrane #status predicted #label TM\
387-468      #domain intracellular #status predicted #label INT\
47-96      #disulfide bonds #status predicted\
55,93,221,245,350      #binding_site carbohydrate (Asn) (covalent) #status
                      predicted\
SUMMARY      #length 468 #molecular-weight 51547 #checksum 4661
Query Match      63.6%; Score 2398; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MLAVGCALLAALLAAGAALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPDNATVHW 60
QY 1 MLAVGCALLAALLAAGAALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPDNATVHW 60
Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 121 CFRKSPNSVVCWEGPRSTPSLTITKAVLLVRKFQNSPAEDFQPCQYSOESQKFSQCLAV 180
QY 121 CFRKSPNSVVCWEGPRSTPSLTITKAVLLVRKFQNSPAEDFQPCQYSOESQKFSQCLAV 180
Db 181 PEGDSSFIYVSMCVASSVSGSFSTQTFQGGIILQDPPANITVTAVARNPRLSVTWQD 240
QY 181 PEGDSSFIYVSMCVASSVSGSFSTQTFQGGIILQDPPANITVTAVARNPRLSVTWQD 240
Db 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVOLRAQEERFQ 300
QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVOLRAQEERFQ 300
Db 301 GEWSEWSPAMGTPTWTSRSPPA 323
QY 301 GEWSEWSPAMGTPTWTSRSPPA 323
RESULT 2
ENTRY      #type complete
TITLE      interleukin-6 receptor precursor (clone lambda p1) - mouse
ORGANISM      #formal name Mus musculus #common_name house mouse
DATE      31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
ACCESSIONS      JLO144
REFERENCE      #authors      Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
                      Hirano, T.; Kishimoto, T.
#journal      J. Exp. Med. (1990) 171:2001-2009
#title      Functional murine interleukin 6 receptor with the
                      intracisternal a particle gene product at its cytoplasmic
                      domain: its possible role in plasmacytomagenesis.
#cross-references      MUID:90278354
#accession      JLO144
#status      #molecule_type mRNA
#residues      1-460 ##label SIG
#cross-references      GDB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
REFERENCE      #experimental_source clone lambda 301
                      SI4543
#authors      Fiorillo, M.T.; Ciliberto, G.; Dente, L.
#submission      submitted to the EMBL Data Library, July 1990
#description      Cloning and expression of murine IL-6 receptor.
#accession      SI4543
#status      #status preliminary
#molecule_type      mRNA
#residues      1-373, 'R', 375-460 ##label FTO
#cross-references      EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
CLASSIFICATION      #superfamily ciliary neurotrophic factor receptor; cytokine

```

```

##residues      1-440 ##label SIG
#cross-references      GDB:X51976; NID:g53548; PIDN:CAA36238.1; PID:g53549
CLASSIFICATION      #superfamily ciliary neurotrophic factor receptor; cytokine
                      receptor homology; immunoglobulin homology
KEYWORDS      cytokine receptor; transmembrane protein
FEATURE
1-19      #domain signal sequence #status predicted #label SIG\
20-440      #product interleukin-6 receptor #status predicted #label
              MAT\
117-306      #domain cytokine receptor homology #label CRS\
358-385      #domain transmembrane #status predicted #label TRA
SUMMARY      #length 440 #molecular-weight 47901 #checksum 5876
Query Match      35.0%; Score 1320; DB 2; Length 440;
Best Local Similarity 55.1%; Pred. No. 7.38e-244;
Matches 179; Conservative 58; Mismatches 82; Indels 6; Gaps 3;
Db 1 MLTVGCTLLVALLAALPAVALVLSGCRALVANGVTVSLPGATVTLICPGKAAGNVIHW 60
QY 1 MLAVGCALLAALLAAGAALAPRCPAQEVARGVLTSLPGDSVLTLCGVEPDNATVHW 60
Db 61 VY---SGSQNRWTTGNTLVLDVQLSDGTYLCSLNDHLVGTVPVLLVDVPPPEPKLS 116
QY 61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 117 CFRKNPLVNAICEWRSPSTPSPTTKAVLFAKKINTNGKSDFOVPCOYSQOLKSFSCQVE 176
QY 121 CFRKSPNSVVCWEGPRSTPSLTITKAVLLVRKFQNSPAE-DFQPCQYSOESQKFSQCLA 179
Db 177 ILEGDKYVHIVSLCVANSVSGSKSHNEAFHSLKMKVDPDPANLVSAIPGRPLWKYSWQ 236
QY 180 VPEGDSSFIYVSMCVASSVSGSFSTQTFQGGIILQDPPANITVTAVARNPRLSVTWQ 239
Db 237 HPETWDSYLLQQLRYRPVNSKEFTVLLLPVAYOCVTHDALRGVHVQVVRGKELD 296
QY 240 DPHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVOLRAQEERFQ 299
Db 297 LGOWSEWSPVETGPTWIAEPRTTPA 321
QY 300 QGEWSEWSPAMGTPTWTSRSPPA 323
RESULT 3
ENTRY      #type complete
TITLE      interleukin-6 receptor precursor (clone lambda 301) - mouse
ORGANISM      #formal name Mus musculus #common_name house mouse
DATE      31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
ACCESSIONS      JLO145; SI4543
REFERENCE      #authors      Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.;
                      Hirano, T.; Kishimoto, T.
#journal      J. Exp. Med. (1990) 171:2001-2009
#title      Functional murine interleukin 6 receptor with the
                      intracisternal a particle gene product at its cytoplasmic
                      domain: its possible role in plasmacytomagenesis.
#cross-references      MUID:90278354
#accession      JLO145
#status      #molecule_type mRNA
#residues      1-460 ##label SIG
#cross-references      GDB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
REFERENCE      #experimental_source clone lambda 301
                      SI4543
#authors      Fiorillo, M.T.; Ciliberto, G.; Dente, L.
#submission      submitted to the EMBL Data Library, July 1990
#description      Cloning and expression of murine IL-6 receptor.
#accession      SI4543
#status      #status preliminary
#molecule_type      mRNA
#residues      1-373, 'R', 375-460 ##label FTO
#cross-references      EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
CLASSIFICATION      #superfamily ciliary neurotrophic factor receptor; cytokine

```

	receptor homology; immunoglobulin homology cytokine receptor; transmembrane protein
KEYWORDS	
FEATURE	
1-19	#domain signal sequence #status predicted #label SIG\
20-460	#product interleukin-6 receptor #status predicted #label MAT\
117-306	#domain cytokine receptor homology #label CRS\
358-385	#domain transmembrane #status predicted #label TRA
SUMMARY	#length 460 #molecular-weight 50454 #checksum 1296
Query Match	35.1%; Score 1320; DB 2; Length 460;
Best Local Similarity	55.1%; Pred. No. 7,38e-244;
Matches 179;	Conservative 58; Mismatches 82; Indels 6; Gaps 3;
Db 1	MLRVGCTLLVALLAAPAVALVIGSCRALEVANGTVTSLPGATVTILCPGKEAGNVTIHW 60
QY 1	MLAVGCALLAALLAAPALPRCPAQEVARGVLTSPLGDSVTLTTCGVEPEDNATVHW 60
Db 61	VY----SGSONREWTITGNLIVRLVDSDTGDLCSLDHLVGVIPLVPPPEPKLS 116
QY 1	: : : : : : : : : : : : : : 116
Db 61	VLRKPAAGSHPSWAGMGRLLRSVQLHDSNGSYCYRAGRPAAGTVHLLDVDPPEPOLLS 120
QY 1	: : : : : : : : : : : : : 120
Db 117	CFRKNLVNAICWRPSSPTTKAVLFPAKKINTNGSKDFQVPCOYSQOLKSFSCOVE 176
QY 1	: : : : : : : : : : : : : 176
Db 121	CFRKSLSNVCWGPRSPSTLTRKAVLVIRFQNSPAB-DQEFCQYQSQSKFSQOLA 179
QY 1	: : : : : : : : : : : : : 179
Db 177	ILEGDKVIHYISLCVANSYGSKSSHNEAFPHSLKMVPDPPANLVVSATPGRPRLKWSWQ 236
QY 1	: : : : : : : : : : : : : 236
Db 180	VPEGDSFYIVSMCVASSVGSKFTQTQGGGILQPDPPANITVAVARNRWLSVTWQ 239
QY 1	: : : : : : : : : : : : : 239
Db 237	HPTWDPSYLLQFLQRPRVSKETVLLLPPVAQCQVIHDALRGVHVQVRKEELD 296
QY 1	: : : : : : : : : : : : : 296
Db 240	DPHSWNSSFYRLFELRYAERSKTETTWMVKDLQHCHVIDAWSGLRHVVQLRAQEFG 299
QY 1	: : : : : : : : : : : : : 299
Db 297	LQOWSESPVETGTPIAPRTTPA 321.
QY 1	: : : : : : : : : : : : : 321
Db 300	QGWESESPAMGPWN-TESRSPA 323
QY 1	: : : : : : : : : : : : : 323
ENTRY	4
TITLE	IVHUB2 #type complete
ALTERNATE_NAMES	interleukin-6 precursor - human
B-factor	cell differentiation factor; B-cell hybridoma growth
C-factor	factor; B-cell stimulating factor 2 (BSF-2); CTL
D-factor	differentiation factor; IL-6; interferon beta-II-a;
E-factor	megakaryocyte potentiation factor
F-factor	
G-factor	
H-factor	
I-factor	
J-factor	
K-factor	
L-factor	
M-factor	
N-factor	
O-factor	
P-factor	
Q-factor	
R-factor	
S-factor	
T-factor	
U-factor	
V-factor	
W-factor	
X-factor	
Y-factor	
Z-factor	
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
ACCESSIONS	A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B27601; A60400; A29085; A61159; A61462; A48419; C48419; B48419; JX0305; S04982
REFERENCE	A32648
#authors	Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.;
#journal	Matsuda, T.; Nakai, S.; Kishimoto, T.
#title	EMBO J. (1987) 6:2939-2945
#cross-references	Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene.
#accession	#cross-references MUID:88082684
#molecule_type	DNA
#residues	1-212 #label YAS
#cross-references	GB:Y00081; NID:g29494; PIDN:CAA68278.1; PID:g29495
#note	the authors translated the codon CAG for residue 130 as Glu
REFERENCE	A91051
#authors	Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
#journal	EMBO J. (1986) 5:2529-2537
#title	Structure and expression of cDNA and genes for human interferon-beta-2, a distinct species inducible by growth-stimulatory cytokines.
#cross-references	MUID:87053818
#accession	A25692
#molecule_type	mRNA
#residues	1-212 #label ZIL
#cross-references	GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674
REFERENCE	A93387
#authors	Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.;
#journal	Matsuda, T.; Kashiwamura, S.I.; Nakajima, K.; Koyama, K.;
#title	Iwamatsu, A.; Tsunawasa, S.; Sakiyama, F.; Matsui, H.;
#cross-references	Nature (1986) 324:73-76
#accession	Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocytes to produce immunoglobulin.
#molecule_type	mRNA
#residues	1-212 #label HIR
#cross-references	GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850
REFERENCE	A33515
#authors	Tanouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
#journal	Biochem. Biophys. Res. Commun. (1989) 163:1056-1062
#title	Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of the mRNA and high-level expression in mouse NIH3T3 cells.
#cross-references	MUID:89391958
#accession	A33515
#molecule_type	mRNA
#residues	1-212 #label TON
#cross-references	GB:M29150; NID:g186349; PIDN:AAA59154.1; PID:g307063
REFERENCE	A25801
#authors	Haegeman, G.; Content, J.; Voicckaert, G.; Derynck, R.;
#journal	Tavernier, J.; Fiers, W.
#title	Eur. J. Biochem. (1986) 159:625-632
#cross-references	Structural analysis of the sequence coding for an inducible 26-kDa protein in human fibroblasts.
#accession	MUID:87004683
#molecule_type	DNA; mRNA
#residues	1-212 #label HAE
#cross-references	GB:X04403
#experimental_source	fibroblast
REFERENCE	A25921
#authors	May, L.T.; Helfgott, D.C.; Sehgal, P.B.
#journal	Proc. Natl. Acad. Sci. U.S.A. (1986) 83:8957-8961
#title	Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts: structural studies of the beta-2 interferon involved.
#cross-references	MUID:87067433
#accession	A25921
#molecule_type	mRNA
#residues	1-212 #label MAY
#cross-references	GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
REFERENCE	I52193
#authors	Wong, G.G.; Wittek-Giannotti, J.; Hewick, R.M.; Clark, S.C.;
#journal	Ogawa, M.
#title	Behring Inst. Mitt. (1988) 83:40-47
#cross-references	Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
#accession	MUID:89193317
#status	preliminary; translated from GB/EMBL/DDBJ

[illegible]

```

##residues 1-212 ##label BRA
##cross-references GB:M18403; NID:g184631; PIDN:AAAS2729.1; PID:g306911
REFERENCE A92816
#authors Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De
Ley, M.; Billiau, A.
#journal J. Immunol. 140:1534-1541
#title Separation and comparison of two monokines with
lymphocyte-activating factor activity: IL-1-beta and
hybridoma growth factor (HGF). Identification of
leukocyte-derived HGF as IL-6.
#cross-references MUID:88154445
#accession A27601
##molecule_type protein
##residues 28-51,'X',53-57,'X',59,'X',61 ##label VAN1
#accession B27601
##molecule_type protein
##residues 30-56,'XX',59-61,'X',63 ##label VA2
REFERENCE A60400
#authors Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
#journal J. Immunol. (1990) 144:1808-1816
#title The human lung fibroblast cell line, MRC-5, produces multiple
factors involved with megakaryocytopoiesis.
#cross-references MUID:90171574
#accession A60400
##molecule_type protein
##residues 30-43 ##label YAM
REFERENCE A29085
#authors Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.;
Takatsuki, F.; Shimizu, M.; Murashima, A.; Tsunasawa, S.;
Sakiyama, F.; Kishimoto, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:228-231
#title Human beta-cell differentiation factor defined by an
anti-peptide antibody and its possible role in autoantibody
production.
#cross-references MUID:87092370
#accession A29085
##molecule_type protein
##residues 29-42 ##label HIR2
REFERENCE A61159
#authors Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.;
Hara, T.; Ishikawa, H.; Arimura, H.; Konno, K.
#journal Anticancer Res. (1991) 11:961-968
#title Purification and characterization of human fibroblast derived
differentiation inducing factor for human monoblastic
leukemia cells identical to interleukin-6.
#cross-references MUID:91290785
#accession A61159
##molecule_type protein
##residues 30-42 ##label NOD
##experimental_source fibroblast
REFERENCE A61462
#authors Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno,
A.
#journal J. Mol. Cell. Immunol. (1989) 4:203-212
#title Interleukin 6 is the principal cytolytic T lymphocyte
differentiation factor for thymocytes in human leukocyte
conditioned medium.
#cross-references MUID:90121567
#accession A61462
##molecule_type protein
##residues 28-48 ##label MIN
##experimental_source leukocyte-conditioned medium
REFERENCE A48419
#authors May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal,
P.B.
#journal Cytokine (1991) 3:204-211
#title Marked cell-type-specific differences in glycosylation of
human interleukin-6.
#cross-references MUID:91355644
#accession A48419
##molecule_type protein
##residues 30-37,'X',39-40 ##label MAY2
##experimental_source FS-4 fibroblasts

```

```

##note sequence extracted from NCBI backbone
##note this 28-30K form contained both N-linked and O-linked
carbohydrate; a 25K form containing only N-linked
carbohydrate was also found
#accession C48419
##molecule_type protein
##residues 28-40 ##label MAY3
##experimental_source FS-4 fibroblasts
##note sequence extracted from NCBI backbone (NCBIP:63787)
##note this 23-25K form contained O-linked but not N-linked
carbohydrate
REFERENCE JX0305
#authors Orita, T.; Oheda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.;
Ochi, N.
#journal J. Biochem. (1994) 115:345-350
#title Polypeptide and carbohydrate structure of recombinant human
interleukin-6 produced in chinese hamster ovary cells.
#cross-references MUID:94266765
#contents annotation; modified sites in recombinant protein from CHO
cells
REFERENCE S04981
...
Note: remainder of annotations omitted.
Query Match 34.1%; Score 1287; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 8,47e-237;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 29 PVPGEISKDVAAPROPLTSSRIDKQIRYLDIGISALRKETCNKSNMCSSEKEALAE 88
|||||
Qy 337 PVPGEISKDVAAPROPLTSSRIDKQIRYLDIGISALRKETCNKSNMCSSEKEALAE 396
|||||
Db 89 NLNPKAEKDCGQSGFNEETCLVKITGLLEFEVILEYLNQNFESSEQARAVQSTK 148
|||||
Qy 397 NLNPKAEKDCGQSGFNEETCLVKITGLLEFEVILEYLNQNFESSEQARAVQSTK 456
|||||
Db 149 VLIQFLOKAKNLDATITPDPTTNASLLTKLQAOQWLODMTTHILRSFEFLQSSLR 208
|||||
Qy 457 VLIQFLOKAKNLDATITPDPTTNASLLTKLQAOQWLODMTTHILRSFEFLQSSLR 516
|||||
Db 209 LRQM 212
|||||
Qy 517 LRQM 520
|||||
RESULT 5 A37986 #type complete
ENTRY interleukin-6 receptor precursor - rat
TITLE IL-6 receptor
ALTERNATE_NAMES #formal_name Rattus norvegicus #common_name Norway rat
ORGANISM 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
DATE 22-Jun-1999
ACCESSIONS A37986
REFERENCE A37986
#authors Baumann, M.; Baumann, H.; Fey, G.H.
#journal J. Biol. Chem. (1990) 265:19853-19862
#title Molecular cloning, characterization and functional expression
of the rat liver interleukin 6 receptor.
#cross-references MUID:91060602
#accession A37986
##molecule_type mRNA
##residues 1-462 ##label BAU
##cross-references GB:M58587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
PID:g204922
COMMENT After binding IL-6, this chain associates with a 130K glycoprotein
that is essential for transmembrane signaling.
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
receptor homology; immunoglobulin homology
KEYWORDS acute phase; cytokine receptor; transmembrane protein
FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
20-462 #product interleukin-6 receptor #status predicted #label
MAY\

```

```
20-362      #domain extracellular #status predicted #label EXT\
40-94      #domain immunoglobulin homology #label IMM\
117-306    #domain cytokine receptor homology #label CRS\
363-385    #domain transmembrane #status predicted #label TM\
386-462    #domain intracellular #status predicted #label INT\
47-92      #disulfide_bonds #status predicted
SUMMARY    #length 462 #molecular-weight 49560 #checks 9669

Query Match      29.0%; Score 1095; DB 1; Length 462;
Best Local Similarity 50.6%; Pred. No. 7.11e-196;
Matches 172; Conservative 58; Mismatches 99; Indels 11; Gaps 7;

Db 1 MLAVGCTLLVALLAAPAVALVGLSCRALEVANGTVTSFGATVTLICPGKEAAGNATIH 60
QY 1 MLAVGCALLAALLAAPGAALAPRCAPAQEVARGVLTSLPGDSVTLCQVPEPDNATVHW 60

Db 61 VY----SGSQSREWTGTVLRAVQVNDTGHYLCFLDDHLVGTVPDLLVDVPPPEPKLS 116
QY 61 VLRKPAAGSHPRWAGMGRRLLRSVQLHDSGNSYCYRAGRAGTGVHLLVDVPPPEPKLS 120

Db 117 CFRKNPLVNAFCWEHPSPSTPTTKAVMFAKKINTTNGKSDFOVPCQYSOQLKSFSCVE 176
QY 121 CFRKSPLSNVCEWGPSPSTPTTKAVLVKRFQNSPAE-DQEPQCYQSQESQKFSQCLA 179

Db 177 ILEGDKVYHIVSLCVANSVGRSSHHNVFQSLKMWQDPDPPANLVSAIPGSLVGRKSVGK 236
QY 180 VPEGDSFFIVSMCVASSVGRKFSKTQTFQGGCILLQDPDPPANITVAVARNPR-WLSVTW 238

Db 237 TUSPGTVTCCNSPFDLYQGR--TFTVWPLVQAQHCQVHDALRGVHVQVVRGKE 294
QY 239 Q-DPHSWNSSFYRLRFELRYAERSKFTFTVMVKDLQHCYVHDASGLRHVVQLRAQEE 297

Db 295 FDIGOWKSPSEVTPGTPPLAEPRTPA-GIPGNPTQVSVE 333
QY 298 FQGEWSEWSPAMGTPW-TESRPPARGGGGGGGGVSVE 336

RESULT 6
ENTRY    #type complete
TITLE    interleukin-6 precursor - horse
ORGANISM #formal_name Equus caballus #common_name domestic horse
DATE     11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
23-Jul-1999
ACCESSION T09216
REFERENCE Z16613
#authors Swiderski, C.E.; Horohov, D.W.
#submission submitted to the EMBL Data Library, July 1996
#accession T09216
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-208 #label SWI
#cross-references EMBL:U64794; NID:g2654387; PID:g2654388

GENETICS
#gene IL-6
#superfamily interleukin-6
#length 208 #molecular-weight 23419 #checks 3370

CLASSIFICATION
#superfamily interleukin-6
#cytokine; growth factor
#length 208 #molecular-weight 23419 #checks 3370

SUMMARY
Query Match      21.4%; Score 806; DB 2; Length 208;
Best Local Similarity 59.2%; Pred. No. 6.02e-135;
Matches 109; Conservative 42; Mismatches 29; Indels 4; Gaps 3;

Db 29 PLPLGSD--E-TTNGPLTTADKTKQHILKILGKTSALKNEMCNFSCENSKVLAEN 85
QY 337 PYPFGSDSKVAAPHRQPLTSSRIDKQIRYILDGISALRKETCNKNMCESSKEALAEN 396

Db 86 NLNLPMKAEKDCFGSGFNQETLMKITTTGLFEFFIYLYLQNEFKGKENTKTMQISTK 145
QY 397 NLNLPMKAEKDCFGSGFNEETCLVKIITGLLEFEVLYLQNRFFESSEQARAVQMSTK 456

Db 146 VLVIQMLQMKKNPE-VTTPDPPTAKSLAKHSQNEWLNKNTTHLILRSLEDFLOQSLRA 204
QY 457 VLITQFLQKAKNLDAITTPDPTNASLLTKLQAQNWQLQDMTTHLILRSFKFELQSSLRA 516
```

```
Db. 205 VRIM 208
QY 517 LRQM 520

RESULT 7
ENTRY    #type complete
TITLE    interleukin 6 - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE     21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
16-Jul-1999
ACCESSION I46590
REFERENCE I46590
#authors Mathialagan, N.; Bixby, J.; Roberts, M.R.
#journal Mol. Reprod. Dev. (1992) 32:324-330
#title Expression of interleukin-6 in porcine, ovine, and bovine
preimplantation conceptuses.
#cross-references MUID:92360284
#accession I46590
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-212 #label MAT
#cross-references GB:M80258; NID:g164514; PIDN:AAC27127.1; PID:g164515

GENETICS
#gene IL-6
#superfamily interleukin-6
#length 212 #molecular-weight 23952 #checks 759

CLASSIFICATION
#superfamily interleukin-6
#length 212 #molecular-weight 23952 #checks 759

SUMMARY
Query Match      21.2%; Score 801; DB 2; Length 212;
Best Local Similarity 59.8%; Pred. No. 6.67e-134;
Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;

Db 34 EDAGKDATSDKMLFTSPDKTEELIKYILGKISAMRKEMCEKYKCNSEKVLAEENLNLP 93
QY 342 EDSKDVAAPHROPLTSSRIDKQIRYILDGISALRKETCNKNMCESSKEALAENLNLP 401

Db 94 KMAEKDGCFCGSGFNQETCLMRITTLGLVEFOIYLDYLOKYEYKNGVNAEAVQISTKALIQ 153
QY 402 KMAEKDGCFCGSGFNEETCLVKIITGLLEFEVLYLQNRFFESSEQARAVQMSTKVLIOF 461

Db 154 LRQKGNPKATTPNPTNAGLLDKLQSQNEWMKNTKIILRSLEDFLOFSURAIRIM 212
QY 462 LQKAKNLDAITTPDPTNASLLTKLQAQNWQLQDMTTHLILRSFKFELQSSLRALQM 520

RESULT 8
ENTRY    #type complete
TITLE    prointerleukin 6 - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE     21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
16-Jul-1999
ACCESSION I46621
REFERENCE I46621
#authors Richards, C.; Saklatva, J.
#journal Cytokine (1991) 3:269-276
#title Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA
and Expression of mRNA in Synovial Fibroblasts In Vitro.
#cross-references MUID:91338547
#accession I46621
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-212 #label RIC
#cross-references GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625

GENETICS
#gene IL6
#superfamily interleukin-6
#length 212 #molecular-weight 23880 #checks 819

CLASSIFICATION
#superfamily interleukin-6
#length 212 #molecular-weight 23880 #checks 819

SUMMARY
Query Match      21.2%; Score 801; DB 2; Length 212;
Best Local Similarity 59.8%; Pred. No. 6.67e-134;
Matches 107; Conservative 37; Mismatches 35; Indels 0; Gaps 0;
```

```
Db 34 EDAGDQATSKMLFTSPDKTEELIKYILKISAMRKECKEYKESKEVLAENNLNP 93
QY 342 EDSKQVAAPHROPLASSERIDQIRYILDGIALRKETCNKSNMCESSKEALAENNLNP 401
Db 94 KMAEKDGCQSGFNQETCLMRITTTGLVFEQIYLDYLOKEYESKNVPAVQISKALIQ 153
QY 402 KMAEKDGCQSGFNEETCLVKIITGLLEFEVLEYLQNRFSSEBQARAVQMSTKVLQ 461
Db 154 LRQKGNPKDATTPTNPTNAGLLDKLOSNEWKMKTKIILILRSLEDFLOSLRAIRM 212
QY 462 LQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSLRALQM 520

RESULT 9
ENTRY A56610 #type complete
TITLE Interleukin-6 precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS A56610; S22162
REFERENCE A56610
#authors Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
#journal DNA Seq. (1992) 2:411-413
#title Nucleotide sequence of bovine interleukin-6 cDNA.
#cross-references MUID:93076003
#accession A56610
#status preliminary
##molecule_type mRNA
##residues 1-208 ##label DRO
##cross-references EMBL:X57317; NID:g2193; PID:CAA40572.1; PID:g2194
##experimental_source BLV induced B cell-lymphosarcoma
#note #sequence extracted from NCBI backbone (NCBIP:118917)
CLASSIFICATION #superfamily interleukin-6
KEYWORDS cytokine
SUMMARY #length 208 #molecular-weight 23758 #checksum 8010

Query Match 18.4%; Score 693; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 1.87e-111;
Matches 93; Conservative 46; Mismatches 39; Indels 4; Gaps 2;

Db 29 PGPLGEDFNKDTTPGRLLTTPKTEALIKRMVKIKISAMRKEICEKNDCESSKETLAEN 88
QY 337 PVPFGEDSKVAAPHROPLTSSERIDQIRYILDGIALRKETCNKSNMCESSKEALAEN 396
Db 89 KLNLPKMEKDCGCGSGFNQALIRTAGLLEYQIYLDYLOKEYEGNQVNRDLRKIR 148
QY 397 NLNLPKMAEKDCGCGSGFNEETCLVKIITGLLEFEVLEYLQNRFSSEBQARAVQMSTK 456
Db 149 TLIQILKOKIADL--ITTP--ATNTDLEKMQSSNEWKNAKIILILRNLENFLQFSLR 204
QY 457 VLIQFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSLR 516
Db 205 IR 206
QY 517 LR 518

RESULT 10
ENTRY I46084 #type complete
TITLE Interleukin 6 - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
ACCESSIONS I46084
REFERENCE I46084
#authors Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
#journal Proc. Soc. Exp. Biol. Med. (1993) 204:301-305
#title Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
#cross-references MUID:94052249
#accession I46084
#status preliminary; translated from GB/EMBL/DBJ
```

```
##molecule_type mRNA
##residues 1-207 ##label BRA
##cross-references GB:LI6914; NID:g438519; PIDN:AAAI6620.1; PID:g438520
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 207 #molecular-weight 23212 #checksum 9069

Query Match 18.0%; Score 680; DB 2; Length 207;
Best Local Similarity 52.3%; Pred. No. 9.08e-109;
Matches 91; Conservative 41; Mismatches 39; Indels 3; Gaps 2;

Db 36 ATSNRLPTPADKMEELIKYILGKISALKKEMCDNKNKCESKEALAENNLNPKLAEKD 95
QY 348 AAPHRQPLTSSERIDQIRYILDGIALRKETCNKSNMCESSKEALAENNLNPKMAEKD 407
Db 96 GCFOSGFGNQETCLRITTTGLOEFOIYLFLOKDYEGDKENAKSVYTSNVLLQMLKRKGK 155
QY 408 GCFOSGFGNEETCLVKIITGLLEFEVLEYLQNRFSSEBQARAVQMSTKVLQFLQKAK 467
Db 156 NODEVTIPVPTVEVGL--QLSCSHRRVAEHNHLLTLRLLEDFLOQLRLRAVRIM 207
QY 468 NLDAITTPDPTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSLRALQM 520

RESULT 11
ENTRY S29549 #type complete
TITLE Interleukin-6 - sheep
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS S29549
REFERENCE S29549
#authors Ebrahimi, B.
#submission submitted to the EMBL Data Library, October 1992
#accession S29549
#status preliminary
##molecule_type mRNA
##residues 1-208 ##label EBR
##cross-references EMBL:X68723
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 208 #molecular-weight 23526 #checksum 7927

Query Match 18.0%; Score 679; DB 1; Length 208;
Best Local Similarity 50.5%; Pred. No. 1.46e-108;
Matches 92; Conservative 43; Mismatches 43; Indels 4; Gaps 2;

Db 29 PGPLGEDFNKDTTPSRLLTTPKTEALIKHIYDKISAIRKEICEKNDCEKSNKETLAEN 88
QY 337 PVPFGEDSKVAAPHROPLTSSERIDQIRYILDGIALRKETCNKSNMCESSKEALAEN 396
Db 89 KLNLPKMEKDCGCGSGFNQAVCLIKTAGLLEYQIYLDYLOKEYEGNQVNRDLQSSIR 148
QY 397 NLNLPKMAEKDCGCGSGFNEETCLVKIITGLLEFEVLEYLQNRFSSEBQARAVQMSTK 456
Db 149 TLIQILKEKIAGL--ITTP--ATHTDLEKMQSSNEWKNAKIILILRSLENFLQFLRL 204
QY 457 VLIQFLQKAKNLDAITTPDPTTNASLLTKLQAOQNLQDM-TTHILRSKFELQSSLR 516
Db 205 IR 206
QY 517 LR 518

RESULT 12
ENTRY ICMS6 #type complete
TITLE Interleukin-6 precursor - mouse
ALTERNATE_NAMES B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte-stimulating factor; IL-6; interferon beta-II; interleukin-HPI; myeloid differentiation inducer MGI-2A; plasmacytoma growth factor
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change
#status 22-Jun-1999
```



```
#Journal      Genomics (1995) 25:157-163
#title        Genomic organization and chromosomal localization of the
              human and mouse genes encoding the alpha receptor component
              for ciliary neurotrophic factor.
#cross-references MUID:95293367
#accession     A56526
#molecule_type DNA
#residues      1-346,'S',348-372 #label VAL
#cross-references GB:L38025; NID:g608654; PIDN:AAA91337.1; PID:g608656
COMMENT        The CNTF receptor is attached to the membrane by a
glycosylphosphatidylinositol anchor.
COMMENT        The CNTF receptor sequence appears to contain several PEST regions.
GENETICS
#gene          GDB:CNTRF
#cross-references GDB:134652; OMIM:118946
#map_position  9p13-9p13
CLASSIFICATION #superfamily ciliary neurotrophic factor receptor; cytokine
              receptor homology; immunoglobulin homology
KEYWORDS       glycoprotein; growth factor receptor; membrane protein;
              phosphatidylinositol linkage
FEATURE
1-20           #domain signal sequence #status predicted #label SIG\
21-372         #product ciliary neurotrophic factor receptor #status
              predicted #label MAT\
39-91          #domain immunoglobulin homology #label IMM\
116-296        #domain cytokine receptor homology #label CRS\
46-89          #disulfide_bonds #status predicted\
60,70,142,190  #binding_site carbohydrate (Asn) (covalent) #status
              predicted
SUMMARY        #length 372 #molecular-weight 40649 #checksum 6224

Query Match      10.8%; Score 408; DB 1; Length 372;
Best Local Similarity 29.9%; Pred. No. 8.89e-54;
Matches 102; Conservative 86; Mismatches 129; Indels 24; Gaps 21;

Db 11 AVLAATAAAVYAAQRHSPQAPHVQYERL-GSDVTLP-C-GT-ANWDAAVTW--RVNGTDIA 65
QY 11 ALAAGAALAPRCAPQAEVARGVLTSLPGDSVTLTCPGVEPEDNATVHWLKRPAAGSH 70

Db 66 PLLNG-SQ-LVLHGLHGLHGLYACFHRDWSHLRHQVLLHVGLPPEPVLS-C-RSNTYP 122
QY 71 PSRWAGMGRRLRLSLVQLHDSGNSCY-RAGRPAGTVHLL-VDPVPEEPQLSCFRKSPLS 128

Db 123 KGFYCSW-HLPTTYIPNT-FNVTVLHGS--KIMV-CE-KDPALKNRCHIRYMHLESTI 175
QY 129 NVV-CEWGRSTPSTLTAKVLYRKFNQSPAEQFQPCQYSQESQKFSQCLAVPEGDSF 187

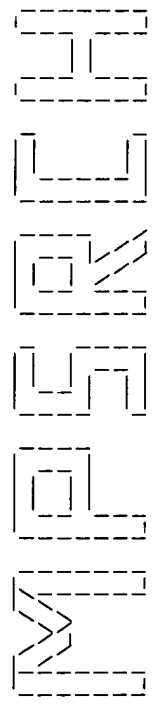
Db 176 KYKVSISVSNALGHN-ATAITDEFITVKPDPPENNVARVPSPNRRLEVLTWQTFSTWPD 234
QY 188 -YIVSMCVASSVGSFKSTQTQFGCGILQPDPPANITVTAVARNPRLSVTWQDPHSW-N 245

Db 235 PSEFPLKFTFLYRPLLDQWQHVLSGDGTAH-TITDAYAGKEYIIQVAAKDN-EIGTWSD 292
QY 246 SSFYRLRFELRYAERSKSTFTTMMYKDLQHHCVIHDAMSGLRHVYVQLRAQEEFGGEWSE 305

Db 293 WSAVAHAATPTEPRHLTEAQAAETTTSTSSLAPPTTK 333
QY 306 WSPFAMGTPWTE-SRSPARGGGGGGGGVPEVPPGEDSK 345
```

Search completed: Thu Aug 10 16:15:17 2000
Job time : 95 secs.

This Page Blank (uspto)



Release 3.1A John F. Collins, BioComputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:19:36 2000; MasPar time 10.55 Seconds
Tabular output not generated. 711.501 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.pep
Perfect Score: 3771
Sequence: 1 MLAVGALLAALLAAPGAAL.....LILRSFKFLQSSLRALRQM 520
Scoring table: PAM 150
Gap 11
Searched: 145341 seqs, 14437480 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1
Statistics: Mean 34.924; Variance 189.856; scale 0.184

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2398	63.6	344	5	5480796-7	3.44e-175
2	2398	63.6	344	5	5171840-7	3.44e-175
3	2398	63.6	468	5	5480796-2	3.44e-175
4	2398	63.6	468	5	5171840-2	3.44e-175
5	2394	63.5	323	5	5480796-6	7.12e-175
6	2394	63.5	323	5	5171840-6	7.12e-175
7	1542	40.9	386	5	5480796-5	7.67e-108
8	1542	40.9	386	5	5171840-5	7.67e-108
9	1337	35.5	317	4	PCT-US95-0	8.45e-92
10	1337	35.5	317	3	US-08-469	8.45e-92
11	1306	34.6	201	5	5171840-11	2.23e-89
12	1289	34.2	186	4	PCT-US94-1	4.74e-88
13	1289	34.2	186	3	US-08-469	4.74e-88
14	1289	34.2	186	1	US-08-165	4.74e-88
15	1289	34.2	186	4	US-07-921	4.74e-88
16	1289	34.2	186	1	PCT-US95-0	4.74e-88
17	1289	34.2	186	1	US-07-632	4.74e-88
18	1289	34.2	186	1	US-07-745	4.74e-88
19	1287	34.1	184	2	US-08-567	6.79e-88
20	1287	34.1	184	1	US-08-567	6.79e-88
21	1287	34.1	184	5	5186931-1	6.79e-88
22	1287	34.1	185	1	US-07-918	6.79e-88
23	1287	34.1	185	1	US-08-246	6.79e-88

24	1287	34.1	185	1	US-08-231-	Sequence 2, Applicatio	6.79e-88
25	1287	34.1	185	2	US-08-766-	Sequence 5, Applicatio	6.79e-88
26	1287	34.1	185	1	US-07-632-	Sequence 1, Applicatio	6.79e-88
27	1287	34.1	185	2	US-08-716-	Sequence 7, Applicatio	6.79e-88
28	1287	34.1	185	5	5186931-2	atent No. 5186931	6.79e-88
29	1287	34.1	185	4	PCT-US93-0	Sequence 2, Applicatio	6.79e-88
30	1287	34.1	187	1	US-07-632-	Sequence 3, Applicatio	6.79e-88
31	1287	34.1	212	1	US-08-792-	Sequence 9, Applicatio	6.79e-88
32	1287	34.1	212	5	5510472-2	atent No. 5510472	6.79e-88
33	1283	34.0	185	1	US-08-231-	Sequence 6, Applicatio	1.39e-87
34	1283	34.0	185	1	US-07-918-	Sequence 6, Applicatio	1.39e-87
35	1283	34.0	185	4	PCT-US93-0	Sequence 6, Applicatio	1.39e-87
36	1279	33.9	183	1	US-08-009-	Sequence 1, Applicatio	2.86e-87
37	1280	33.9	184	2	US-08-693-	Sequence 2, Applicatio	2.39e-87
38	1280	33.9	184	2	US-09-008-	Sequence 2, Applicatio	2.39e-87
39	1277	33.9	185	1	US-08-231-	Sequence 4, Applicatio	4.10e-87
40	1277	33.9	185	1	US-07-918-	Sequence 4, Applicatio	4.10e-87
41	1277	33.9	185	4	PCT-US93-0	Sequence 4, Applicatio	4.10e-87
42	1273	33.8	185	4	PCT-US93-0	Sequence 8, Applicatio	8.41e-87
43	1273	33.8	185	1	US-08-231-	Sequence 8, Applicatio	8.41e-87
44	1273	33.8	185	1	US-07-918-	Sequence 8, Applicatio	8.41e-87
45	1261	33.4	186	1	US-08-209-	Sequence 2, Applicatio	7.27e-86

ALIGNMENTS

RESULT 1

ID 5480796-7 STANDARD; PRT; 344 AA.

XX xxxxxx

XX Patent No. 5480796

XX Patent No. 5480796

CC APPLICANT: KISHIMOTO, TADAMITSU

CC TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

CC FOR HUMAN B CELL STIMULATORY FACTOR-2

CC NUMBER OF SEQUENCES: 8

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/907,650

CC FILING DATE: 02-JUL-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 298,694

CC FILING DATE: 19-JAN-1989

CC SEQ ID NO:7:

CC LENGTH: 344

CC SEQUENCE 344 AA; 38047 MW; 637889 CN;

Query Match 63.6%; Score 2398; DB 5; Length 344;

Best Local Similarity 100.0%; Pred. No. 3.44e-175;

Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGALLAALLAAPGAALAPRRCPAQEVARGLTSLPGDSVTLTCPCGVEPDNATVHW 60

Qy 1 MLAVGALLAALLAAPGAALAPRRCPAQEVARGLTSLPGDSVTLTCPCGVEPDNATVHW 60

Db 61 VLURKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNYSYRAGRAGTAVHLLVDPVPEPQLS 120

Qy 61 VLURKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNYSYRAGRAGTAVHLLVDPVPEPQLS 120

Db 121 CPERKPLSNVNCWEWGRPSLTTKAVLLVRKFQNSPAEDFOEPCOYSOESOKFSCOLAV 180

Qy 121 CPERKPLSNVNCWEWGRPSLTTKAVLLVRKFQNSPAEDFOEPCOYSOESOKFSCOLAV 180

Db 181 PGEDSSFIVSMCVASSVSGSKFSTQTFCGCGILOPDPANITVTAVARNRWLSVTWQD 240

Qy 181 PGEDSSFIVSMCVASSVSGSKFSTQTFCGCGILOPDPANITVTAVARNRWLSVTWQD 240

Db 241 PHSWNSSFYRLRFELRYRAERSKTTFTTMVKDLQHHCVTHDAWSGLRHVVQLRAQEEFQ 300

Qy 241 PHSWNSSFYRLRFELRYRAERSKTTFTTMVKDLQHHCVTHDAWSGLRHVVQLRAQEEFQ 300

Db	301	GEWSEWSPEAMGTPWTESRPPA	323
Qy	301	GEWSEWSPEAMGTPWTESRPPA	323

RESULT 2
ID 5171840-7 STANDARD; PRT; 344 AA.

Patent No. 5171840

Patent No. 5171840

APPLICANT: KISHIMOTO, TADAMITSU

TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

STIMULATORY FACTOR-2

NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/298,694

FILING DATE: 19-JAN-1989

SEQ ID NO:7:

LENGTH: 344

SEQUENCE 344 AA: 38047 MW: 637889 CN:
LENGTH: 344

Query Match 63.68: Score 2398: DB 5: Length 344.

Query MacCII 63.6%; Score 2398; DB 5; Length 344;
Best Local Similarity 100.0%; Pred NO 3 44e-175.

```

Matches 323: Conservative 0: Mismatches 0: Indels 0: Cans 0:
Best Local Similarity 100.0%; Pred. No. 3.44e-1/5;

```

Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCPGVEPEDNATVHW 60

[illegible]

db 61 VLRKPAAGSHPSRWAGMGRLLLRVQLHDSGNYSYRAGRAGTVHLLVDVPPPEEPOLS 120

[illegible]

Db 121 CFRKSPLSNVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFQEPCCQYSQESQKFSQCLAV 180

[illegible]

Db 181 PEGDSSFYIVSMCVASSVGSKFSTQTFQCGGILQDPFPANITVTAVARNPRWLSVTWOD 240

04Z QDMTASCTMYJNYVAYETATMTUTDTQTCTCCQXTTXRNDTHROCAEDNAHRSATTTTTTTT

Db 241 PHSWNSSFYRLRFELRYRAERSKTFTTMMVKDLOHHCVIHDAWSGLRHVVOLRAOEFEFG 300

22 241 1 MONASOT 1 AKREI EEENIRAKERSRIF IIMV RDLQHHCV IHDAWSGLRHVVQLRAQEFGQ 300

Db 301 GEWSEWSP EAMGTPWTE SRSPPA 323

DD
JOT
GEMSENFEMOIFWIESKSPFA 323

RESULT 3
ID 5480796-2 STANDARD; PRT; 468 AA.

Patent No. 5480796

Patent No. 5480796

PATENT NO.: 3480796
APPLICANT: KISHIMOTO TADAMITSU

APPLICANT: KISHIMOTO, TADAMITSU
TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

III OF INVENTION: ANTIBODIES AGAINST HUMAN B CELL STIMULATORY FACTOR-2

NUMBER OF SEQUENCES: 8

NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/07/907-650

APPLICATION NUMBER: US/
FILING DATE: 02-III-1992

DE	Patent No.	5171840
xx		
CC	Patent No.	5171840
CC	APPLICANT:	KISHIMOTO, TADAMITSU
CC	TITLE OF INVENTION:	RECEPTOR PROTEIN FOR HUMAN B CELL
CC	STIMULATORY FACTOR-2	
CC	NUMBER OF SEQUENCES:	11
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/298,694
CC	FILING DATE:	19-JAN-1989
CC	SEQ ID NO:6:	
CC	LENGTH:	323
CC	SEQUENCE	323 AA; 35744 MW; 577074 CN;
Query Match	63.5%;	Score 2394; DB 5; Length 323;
Best Local Similarity	100.0%;	Pred. No. 7.12e-175;
Matches	322; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1	M LAVGCCALLAALAAAGAAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Qy	1	M LAVGCCALLAALAAAGAAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db	61	VLRKPAAGSHPSRWAGMGRLLRLLSVOLHDSGNYSYRAGRPAAGTVHLLVDVPPEEPQLS 120
Qy	61	VLRKPAAGSHPSRWAGMGRLLRLLSVOLHDSGNYSYRAGRPAAGTVHLLVDVPPEEPQLS 120
Db	121	CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFONSFAEDFOEPCOYSQESQKFSCOLAV 180
Qy	121	CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFONSFAEDFOEPCOYSQESQKFSCOLAV 180
Db	181	PEGDSSFYIIVSMCVASSVGSKFSTQTFCGGILQPDPANITVTAVARNPRLSVTWQD 240
Qy	181	PEGDSSFYIIVSMCVASSVGSKFSTQTFCGGILQPDPANITVTAVARNPRLSVTWQD 240
Db	241	PHSNSSFYRLRFELRYRAERSKTFTTMWKDLQHHCVIHDMSGLRHVVQLRAQEFGQ 300
Qy	241	PHSNSSFYRLRFELRYRAERSKTFTTMWKDLQHHCVIHDMSGLRHVVQLRAQEFGQ 300
Db	301	GEWSESPFAMGTPTWTSRPP 322
Qy	301	GEWSESPFAMGTPTWTSRPP 322
RESULT	7	
ID	5480796-5	STANDARD; PRT; 386 AA.
XX		
AC	xxxxxx	
XX		
DT		
XX		
DE	Patent No.	5480796
XX		
CC	Patent No.	5480796
CC	APPLICANT:	KISHIMOTO, TADAMITSU
CC	TITLE OF INVENTION:	ANTIBODIES AGAINST THE RECEPTOR PROTEIN
CC	FOR HUMAN B CELL STIMULATORY FACTOR-2	
CC	NUMBER OF SEQUENCES:	8
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/907,650
CC	FILING DATE:	02-JUL-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	298,694
CC	FILING DATE:	19-JAN-1989
CC	SEQ ID NO:5:	
CC	LENGTH:	386
CC	SEQUENCE	386 AA; 42734 MW; 827023 CN;
Query Match	40.9%;	Score 1542; DB 5; Length 386;
Best Local Similarity	98.1%;	Pred. No. 7.67e-108;
Matches	212; Conservative	0; Mismatches 0; Indels 4; Gaps 2;
Db	28	VDVPPEEPQLSCFRKSPLSNVVC--GPRSTPWNSLTTKAVLLVRKFONSFAEDFOEPCQY 85

DE Sequence 163, Application US/08469318
XX
CC Sequence 163, Application US/08469318
CC Patent No. 6022535
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
CC TITLE OF INVENTION: Protein
CC NUMBER OF SEQUENCES: 196
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/469,318
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/446,872
CC FILING DATE:
CC INFORMATION FOR SEQ ID NO: 163:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 34.2%; Score 1289; DB 3; Length 186;
Best Local Similarity 98.9%; Pred. No. 4.74e-88;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGSDKDVAAHPHQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 60
QY 335 VEPVPPGSDKDVAAHPHQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 394
Db 61 ENNLNPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 120
QY 395 ENNLNPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 454
Db 121 TKVLIQFLOKAKKALNDAITTPDPTTNASLTKLQAQNWQLDMTTHILRSFKFEFLQSSL 180
QY 455 TKVLIQFLOKAKKALNDAITTPDPTTNASLTKLQAQNWQLDMTTHILRSFKFEFLQSSL 514
Db 181 RALRQM 186
QY 515 RALRQM 520

RESULT 14
ID US-08-165-301A-20 STANDARD; PRT; 186 AA.

XX
AC
XX
XX
DT
XX
DE
XX
XX

Sequence 20, Application US/08165301A

Sequence 20, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:

APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.

CC STREET: 87 CambridgePark Drive
CC CITY: Cambridge
CC STATE: Massachusetts
CC COUNTRY: U.S.A.
CC ZIP: 02140
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,301A
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Meiner, M. C.
CC REGISTRATION NUMBER: 33,544
CC REFERENCE/DOCKET NUMBER: GI 5188D
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 876-1170
CC TELEFAX: (617) 876-5851
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 34.2%; Score 1289; DB 1; Length 186;
Best Local Similarity 98.9%; Pred. No. 4.74e-88;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGSDKDVAAHPHQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 60
QY 335 VEPVPPGSDKDVAAHPHQPLTSSERIDKQIRYILDGISALRKETCNKNMCESSKEALA 394
Db 61 ENNLNPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 120
QY 395 ENNLNPKMAEKDGCFSQGFNEETCLVKIITGLLEFEVILEYLNRFESSEEQARAVQMS 454
Db 121 TKVLIQFLOKAKKALNDAITTPDPTTNASLTKLQAQNWQLDMTTHILRSFKFEFLQSSL 180
QY 455 TKVLIQFLOKAKKALNDAITTPDPTTNASLTKLQAQNWQLDMTTHILRSFKFEFLQSSL 514
Db 181 RALRQM 186
QY 515 RALRQM 520

RESULT 15
ID US-07-921-848-20 STANDARD; PRT; 186 AA.

XX
AC
XX
XX
DT
XX
DE
XX
XX

Sequence 20, Application US/07921848

Sequence 20, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:

APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.

CC ZIP: 02140
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/921,848
CC FILING DATE: 19920728
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/652,531
CC FILING DATE: 06-FEB-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/745,382
CC FILING DATE: 14-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Cseir, Luann
CC REGISTRATION NUMBER: 31,822
CC REFERENCE/DOCKET NUMBER: GI5188A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 876-1170
CC TELEFAX: (617) 876-5851
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 186 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 186 AA; 21112 MW; 171066 CN;

Query Match 34.2%; Score 1289; DB 1; Length 186;
Best Local Similarity 98.9%; Pred. No. 4,74e-88;
Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGIALRKETCNKSNMCSSKEALA 60
QY : |||||
335 VEPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGIALRKETCNKSNMCSSKEALA 394
|||
Db 61 ENNLNLPKMAEKDGCFCGNEETCLVKIITGLLEFEVYLEYLNRFESSEEQARAVQMS 120
QY |||||
395 ENNLNLPKMAEKDGCFCGNEETCLVKIITGLLEFEVYLEYLNRFESSEEQARAVQMS 454
|||
Db 121 TKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHILRSFKFLOSSL 180
QY |||||
455 TKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHILRSFKFLOSSL 514
|||
Db 181 RALRQM 186
QY |||||
515 RALRQM 520

Search completed: Thu Aug 10 16:20:27 2000
Job time : 51 secs.

This Page Blank (usp10)

W P S R L

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:12:21 2000; MasPar time 16.72 Seconds
Tabular output not generated.
736.510 Million cell updates/sec

Title: >US-09-142-471-4
Description: (1-520) from US09142471.ppe
Perfect Score: 3771
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSKFLOSSLRALRQM 520
Scoring table: PAM 150
Gap 11
Searched: 188963 seqs, 23686106 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq36
1:geneseqp
Statistics: Mean 37.159; Variance 190.226; scale 0.195

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	3716	98.5	525	1	W36846 Human fusion polypepti	7.34e-296
2	3458	91.7	543	1	W03164 Chimeric sIL-6R/IL-6 p	3.62e-274
3	3390	89.9	500	1	W36847 Human fusion polypepti	1.88e-268
4	2398	63.6	344	1	P90528 B cell stimulating fac	3.10e-185
5	2398	63.6	468	1	R37215 IL-6 receptor.	3.10e-185
6	2398	63.6	468	1	P90284 Sequence of a receptor	3.10e-185
7	2391	63.4	360	1	W70804 Amino acid sequence of	1.19e-184
8	2392	63.4	468	1	W98364 Interleukin-6 receptor	9.84e-185
9	2390	63.4	468	1	P90525 B cell stimulating fac	1.45e-184
10	2391	63.4	592	1	W70797 Human interleukin-6R-a	1.19e-184
11	2373	62.9	468	1	W71371 Human interleukin-6 re	3.83e-183
12	2351	62.3	323	1	P90527 B cell stimulating fac	2.66e-181
13	2317	61.4	315	1	W70805 Amino acid sequence of	1.86e-178
14	2110	56.0	1042	1	R70122 IL-8 type 1-GPB 130 f	3.77e-161
15	1534	40.7	386	1	P90526 B cell stimulating fac	3.78e-113
16	1368	36.3	182	1	W00403 Interleukin-6 antagoni	2.24e-99
17	1320	35.0	460	1	R13318 IL-6R for soluble IL-6	2.12e-95
18	1311	34.8	460	1	R13318 IL-6 receptor.	1.18e-94
19	1289	34.2	186	1	P80270 Recombinant interleuki	7.79e-93
20	1289	34.2	186	1	R75765 Human interleukin-6.	7.79e-93
21	1287	34.1	184	1	R03914 Polypeptide with human	1.14e-92
22	1287	34.1	184	1	R52556 Interleukin 6.	1.14e-92
23	1287	34.1	184	1	P81158 Polypeptide with B-cel	1.14e-92

24	1287	34.1	184	1	R20783 Interleukin-6.	1.14e-92
25	1287	34.1	184	1	R54990 Mutant Interleukin 6 S	1.14e-92
26	1287	34.1	184	1	W02609 Interleukin-6.	1.14e-92
27	1287	34.1	184	1	R06532 Human B-cell simulator	1.14e-92
28	1287	34.1	184	1	R06623 B-cell differentiation	1.14e-92
29	1287	34.1	185	1	R05274 Segment of human B cel	1.14e-92
30	1287	34.1	185	1	W00130 Human interleukin-6 fr	1.14e-92
31	1287	34.1	185	1	R05275 Segment of human B cel	1.14e-92
32	1287	34.1	185	1	R68624 Ala-BCDF.	1.14e-92
33	1287	34.1	187	1	R13471 hIL-6 protein.	1.14e-92
34	1287	34.1	188	1	R35011 Human interleukin-6 (I	1.14e-92
35	1287	34.1	208	1	P81160 Polypeptide with B-cel	1.14e-92
36	1287	34.1	212	1	R05415 Human B-cell different	1.14e-92
37	1287	34.1	212	1	P70238 Interferon-beta 2a.	1.14e-92
38	1287	34.1	212	1	R72317 Interferon-beta2A.	1.14e-92
39	1287	34.1	212	1	R49041 Human interleukin-6.	1.14e-92
40	1287	34.1	212	1	P90371 PBSF2-L8	1.14e-92
41	1287	34.1	212	1	R49249 Sequence of human B-ce	1.14e-92
42	1287	34.1	212	1	R33430 IFN-beta-2a.	1.14e-92
43	1287	34.1	212	1	R34726 Human IL-6 (for modifi	1.14e-92
44	1287	34.1	212	1	P90047 PBSF2-L8 sequence	1.14e-92
45	1287	34.1	212	1	P90436 Interferon-beta-2.	1.14e-92

ALIGNMENTS

RESULT 1
ID W36846 standard; Protein; 525 AA.
AC W36846; (first entry)
DT 25-MAR-1998
DE Human fusion polypeptide H-IL-6 with 18 amino acid linker.
KW Interleukin-6; IL-6; Interleukin-6 receptor; IL-6R; ligand; conjugate;
KW protein interaction; therapeutic; antagonist.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal_peptide
FT Protein 20..524
FT /note= "H-IL-6 fusion polypeptide"
FT Region 324..341
FT /label= linker region
FT /note= "Links together COOH-terminus of sIL-6R with the NH2-terminus of IL-6"

W09732891-A2.
12-SEP-1997.
07-MAR-1997; D00458.
07-MAR-1996; DE-008813.
PA (ANGE-) ANGEMWANTE GENTECNOLOGIE SYSTEME GMBH.
PI Rose-John S;
DR WPI: 97-470536/43.
DR N-PSDB; T97848.
DR Conjugate of two peptide(s) with mutual affinity connected by a
PT linker - used to modulate interactions between proteins, e.g. for ex
PT vivo expansion of human stem cells
PS Disclosure; Fig 1; 19pp; German.
CC This sequence represents the fusion polypeptide H-IL-6 which contains
CC an 18 amino acid linker which joins the carboxy terminus of human
CC interleukin-6 receptor (IL-6R) with the amino terminus of human
CC interleukin-6 (IL-6). Such conjugates could be used to modulate
CC interactions between proteins, particularly to overcome interrupted
CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
CC constructs derived from IL-6 and its receptor, can also be used for ex
CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
CC antagonist.
SQ Sequence 525 AA;

Query Match 98.5%; Score 3716; DB 1: Length 525;
Best Local Similarity 99.0%; Pred. No. 7.34e-296;
Matches 520; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Db 1 MLAVGCALLAALLAAPGAALPRRCPAQEVARGVLTSLPGDSVTLTCPCVPEPNATVHW 60
|||||

QY 1 MLAVGCALLAALAAAPCAALAPRRCPAQEVARGLTSLPGDSVTLTLCPCGVEPEDNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRAGTGTVHLLVDVPPPEPQLS 120
 QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRAGTGTVHLLVDVPPPEPQLS 120
 Db 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180
 QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180
 Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNRMLSVTWQD 240
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNRMLSVTWQD 240
 Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAGSLRHVVQLRAQEEFG 300
 QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAGSLRHVVQLRAQEEFG 300
 Db 301 GEWSEWPEAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
 QY 301 GEWSEWPEAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
 Db 361 TSSERIDQIRYILDGSLARKETCNKSNMCESSKEALAEANNLNLPMKAEKDCGFSQGFN 420
 QY 361 TSSERIDQIRYILDGSLARKETCNKSNMCESSKEALAEANNLNLPMKAEKDCGFSQGFN 420
 Db 421 EETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVOMSTKVLIQFLQKAKNLDAITTP 480
 QY 421 EETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVOMSTKVLIQFLQKAKNLDAITTP 480
 Db 481 DPTTNASLLTKLAQONQWLDMTTHLLRSFKFLOSSLRALROM 525
 QY 476 DPTTNASLLTKLAQONQWLDMTTHLLRSFKFLOSSLRALROM 520

RESULT 2
 ID Y03164 standard; protein; 543 AA.
 AC Y03164;
 DT 11-JUN-1999 (first entry)
 DE Chimeric sIL-6R/IL-6 protein.
 KW Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6;
 KW chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;
 KW highly malignant cancer cell; in vivo engraftment; mammalian cancer;
 KW human haematopoietic cell; bone marrow transplantation; mammalian cancer;
 KW hepatotoxic agent protection; haematopoiesis; liver disorder;
 KW neurological disorder.
 OS Synthetic.
 PN WO902552-A2.
 PD 21-JAN-1999.
 PF 09-JUL-1998; IL0321.
 PR 30-DEC-1997; IL-122818.
 PR 10-JUL-1997; IL-121284.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Chebeth J, Kollet O, Lapidot T, Revel M;
 DR WPL: 99-120776/10
 PT New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for
 PT e.g. treating cancers, bone marrow transplantation, increasing
 PT haematopoiesis or treating liver or neurological disorders
 PS Claim 6; Fig 3; 77pp; English.
 CS This sequence represents the chimeric glycosylated soluble interleukin-6
 CC receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R/IL-6) of the
 CC invention. It comprises a fusion protein product between all of the
 CC naturally occurring form of sIL-6R and all of the naturally occurring
 CC form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a
 CC similar fashion to the glycosylation of naturally occurring sIL-6R and
 CC IL-6. The sIL-6R/IL-6 and analogues are capable of inhibiting the
 CC growth of highly malignant cancer cells, e.g. melanoma cells, eliciting
 CC the in vivo engraftment of human haematopoietic cells in bone marrow
 CC transplantation and protecting liver from hepatotoxic agents.
 CC They can be used for the preparation of a medicament for treating
 CC mammalian cancers by way of inhibition of cancer cells, for enhancement
 CC of bone marrow transplantation by way of eliciting engraftment of human
 CC haematopoietic cells in bone marrow transplantation, for increasing

CC haematopoiesis, for treating liver or neurological disorders, or in other
 CC applications in which IL-6 or sIL-6R are used.
 SQ Sequence 543 AA;
 Query Match 91.7%; Score 3458; DB 1; Length 543;
 Best Local Similarity 94.1%; Pred. No. 3.62e-274;
 Matches 511; Conservative 3; Mismatches 6; Indels 23; Gaps 4;
 Db 1 MLAVGCALLAALAAAPCAALAPRRCPAQEVARGLTSLPGDSVTLTLCPCGVEPEDNATVHW 60
 QY 1 MLAVGCALLAALAAAPCAALAPRRCPAQEVARGLTSLPGDSVTLTLCPCGVEPEDNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRAGTGTVHLLVDVPPPEPQLS 120
 QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSYRAGRAGTGTVHLLVDVPPPEPQLS 120
 Db 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180
 QY 121 CFRKSPLSNVVCEWGPSTPSLTAKVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180
 Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNRMLSVTWQD 240
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNRMLSVTWQD 240
 Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAGSLRHVVQLRAQEEFG 300
 QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCIVHDAGSLRHVVQLRAQEEFG 300
 Db 301 GEWSEWPEAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
 QY 301 GEWSEWPEAMGTPWTESRPPARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 360
 Db 361 VPEGDSKDVAAAPHROPLTSSERIDQIRYILDGSLARKETCNKSNMCESSKEALAEANN 420
 QY 361 VPEGDSKDVAAAPHROPLTSSERIDQIRYILDGSLARKETCNKSNMCESSKEALAEANN 420
 Db 421 LNLPMKAEKDCGFSQGFNEETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVOMSTKV 480
 QY 421 LNLPMKAEKDCGFSQGFNEETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVOMSTKV 480
 Db 481 LIQFLQKAKNLDAITTPDPTTNASLLTKLAQONQWLDMTTHLLRSFKFLOSSLRAL 540
 QY 481 LIQFLQKAKNLDAITTPDPTTNASLLTKLAQONQWLDMTTHLLRSFKFLOSSLRAL 540
 Db 541 ROM 543
 QY 518 ROM 520
 RESULT 3
 ID W36847 standard; Protein; 500 AA.
 AC W36847;
 DT 25-MAR-1998 (first entry)
 DE Human fusion polypeptide H-IL-6 with 13 amino acid linker.
 KW Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 KW protein interaction; therapeutic; antagonist.
 OS Synthetic.
 OS Homo sapiens.
 FH Key
 FH Location/Qualifiers
 FT Peptide
 FT 1..119
 FT /label= signal_peptide
 FT Protein
 FT 20..500
 FT /note= "H-IL-6 fusion polypeptide"
 FT Region
 FT 304..316
 FT /label= linker region
 FT /note= "Links together COOH-terminus of sIL-6R with
 FT the NH2-terminus of IL-6"
 PN WO9732891-A2.
 PD 12-SEP-1997.
 PF 07-MAR-1997; D00458.
 PR 07-MAR-1996; DE-008813.
 PA (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
 PI Rose-John S;

DR WPI; 97-470536/43.
 DR N-PSDB; T97849.
 PT Conjugate of two peptide(s) with mutual affinity connected by a
 PT linker - used to modulate interactions between proteins, e.g. for ex
 PT vivo expansion of human stem cells
 PS Disclosure; Fig 2; 19pp; German.
 CC This sequence represents the fusion polypeptide H-IL-6 which contains
 CC an 13 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist.
 SQ Sequence 500 AA;

Query Match 89.9%; Score 3390; DB 1; Length 500;
 Best Local Similarity 96.2%; Pred. No. 1.88e-268;
 Matches 500; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Db 1 MLAVGCCALLAALAAAPCAALAPRCAPAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW 60
 QY 1 MLAVGCCALLAALAAAPCAALAPRCAPAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW 60
 Db 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 QY 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 121 CFRKPSLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQSKFSCQLAV 180
 QY 121 CFRKPSLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQSKFSCQLAV 180
 Db 181 PEGDSSFYIYVMCVASSVSGSKFTQTFQCGIILQPPPANITVAVARNPRLSVTWQD 240
 QY 181 PEGDSSFYIYVMCVASSVSGSKFTQTFQCGIILQPPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSNWSFYRLRFELRYRAERSKFTFTMWVKDLQHCVIHDWSGLRHVVQLRAQEEFG 300
 QY 241 PHSNWSFYRLRFELRYRAERSKFTFTMWVKDLQHCVIHDWSGLRHVVQLRAQEEFG 300
 Db 301 GENSEWPEAMGTPWTESRSPPA 323
 QY 301 GENSEWPEAMGTPWTESRSPPA 323

RESULT 4
 ID P90528 standard; protein; 344 AA.
 AC P90528;
 DE B cell stimulating factor-2 receptor.
 KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
 OS Homo sapiens.
 PN A08928720-A.
 PF 27-JUL-1989.
 PR 23-JAN-1989; 028720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadimitsu Kishimoto.

PI Kishimoto T;
 DR WPI; 89-264012/37.
 DR N-PSDB; P90525.
 PT Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders.
 PS Claim 7; page 40; 76pp; English.
 CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
 CC is derived from a monocytic U937 cell line. It can be used to develop
 CC prophylactic and therapeutic pharmaceuticals, as agents to relate
 CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
 CC study an immune mechanism with which BSF-2 or the receptor is concerned.
 SQ Sequence 344 AA;

Query Match 63.6%; Score 2398; DB 1; Length 344;
 Best Local Similarity 100.0%; Pred. No. 3.10e-185;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCCALLAALAAAPCAALAPRCAPAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW 60
 QY 1 MLAVGCCALLAALAAAPCAALAPRCAPAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW 60
 Db 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 QY 61 VLKPPAAGSHPSRWAGMRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 121 CFRKPSLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQSKFSCQLAV 180
 QY 121 CFRKPSLSNVVCEWGPSTSLTAKVLLVRKFNQSPAEFQEPQYQSQSKFSCQLAV 180
 Db 181 PEGDSSFYIYVMCVASSVSGSKFTQTFQCGIILQPPPANITVAVARNPRLSVTWQD 240
 QY 181 PEGDSSFYIYVMCVASSVSGSKFTQTFQCGIILQPPPANITVAVARNPRLSVTWQD 240
 Db 241 PHSNWSFYRLRFELRYRAERSKFTFTMWVKDLQHCVIHDWSGLRHVVQLRAQEEFG 300
 QY 241 PHSNWSFYRLRFELRYRAERSKFTFTMWVKDLQHCVIHDWSGLRHVVQLRAQEEFG 300
 Db 301 GENSEWPEAMGTPWTESRSPPA 323
 QY 301 GENSEWPEAMGTPWTESRSPPA 323

RESULT 5
 ID R37215 standard; Protein; 468 AA.
 AC R37215; 1993 (first entry)
 DE IL-6 receptor.
 KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
 KW transmembrane; multiple myeloma; binding; ability; signal transfer;
 KW disease; intracellular.
 OS Synthetic.
 PN J0501892-A.
 PD 16-APR-1993.
 PF 02-OCT-1991; 255521.
 PR 02-OCT-1991; JP-255521.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PA (KISH/) KISHIMOTO C.
 PA (TOI)) TOSOH CORP.
 DR WPI; 93-161739/20.
 DR N-PSDB; Q41746.
 PT New interleukin-6 receptor deriv. - for treating diseases caused
 PT by IL-6, e.g. multiple myeloma
 PS Disclosure; Page 10-12; 23pp; Japanese.
 CC This sequence represents an interleukin-6 (IL-6) receptor. Variants
 CC of the receptor lacking either the immunoglobulin-like domain or the
 CC transmembrane and intracellular domain have IL-6 binding ability and
 CC signal transfer ability. Either the full length or truncated IL-6
 CC receptors may be used for diseases caused by IL-6 such as multiple
 CC myeloma.
 SQ Sequence 468 AA;

Query Match 63.6%; Score 2398; DB 1; Length 468;

```

Best Local Similarity 100.0%; Pred. No. 3.10e-185;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSLVTLCPCGVPEPDNATVHW 60
   |||||
QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSLVTLCPCGVPEPDNATVHW 60
   |||||

Db 61 VLKRPAGSHPSRWAGMGRRLRLLSVOLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
   |||||
QY 61 VLKRPAGSHPSRWAGMGRRLRLLSVOLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
   |||||

Db 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSOESKFSQCLAV 180
   |||||
QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSOESKFSQCLAV 180
   |||||

Db 181 PEGDSFFIYVSMCVASSVSGSKFSTQTFQCGILQDPDPANITVTAVANPRWLSTWQD 240
   |||||
QY 181 PEGDSFFIYVSMCVASSVSGSKFSTQTFQCGILQDPDPANITVTAVANPRWLSTWQD 240
   |||||

Db 241 PHSWNSFYRLRFLRYRAERSKTFFTTMVKDLOHHCVIHDWSGLRHVVQLRAQEEFGQ 300
   |||||
QY 241 PHSWNSFYRLRFLRYRAERSKTFFTTMVKDLOHHCVIHDWSGLRHVVQLRAQEEFGQ 300
   |||||

Db 301 GEWSESPAMGTPWTESRPPA 323
   |||||
QY 301 GEWSESPAMGTPWTESRPPA 323
   |||||

RESULT 6
ID P90284 standard; Protein; 468 AA.
AC AC
DE 31-MAR-1992 (first entry)
DT Sequence of a receptor protein for human B cell stimulating
DE factor-2 (BSF2 receptor).
KW B cell; immune disorder; therapy; diagnosis; prophylaxis.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
   2..22
   /label= hydrophobic region
   362..386
   /label= hydrophobic region
FT EP-325474-A.
PN PD
PD 26-JUL-1989.
PF 20-JAN-1989; 300536.
PF 22-JAN-1988; JP-012387.
PR 25-JAN-1988; JP-012599.
PR 04-AUG-1988; JP-194865.
PR 14-JAN-1989; JP-017461.
PR 20-JAN-1989; JP-009774.
PP (KISH)/ KISHIMOTO T.
PA Kishimoto T.
PI PI
DR WPI; 89-214667/30.
DR N-PSDB; N90340.
DR Receptor protein for human B cell stimulating factor-2 - obtd. by
PT recombinant DNA techniques and used as diagnostic, prophylactic or
PT therapeutic agent
PT Claim 2; Page 19-21; 63pp; English.
PS The cDNA in N90340 was derived from monocyte cell line U937.
CCC Isolated BSF2 receptor and DNA encoding it are claimed, as are
CCC (b) expression vectors; (c) host organisms; (d) antibodies; and
CCC (e) hybridomas.
SQ Sequence 468 AA;

```

	Query Match	63.6%	Score 2398;	DB 1;	Length 468;
	Best Local Similarity	100.0%;	Pred.	Nm.	3.10e-185;
	Matches	323; Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
Ddb	1	MLAVGCALLAALLAAPGAALAPRCPAQAEVARGVLTLSPGDSTLTCGPVEPDNATVHW	60		
OY	1	MLAVGCALLAALLAAPGAALAPRCPAQAEVARGVLTLSPGDSTLTCGPVEPDNATVHW	60		
Ddb	61	VLRFPAGSHPSRWAGMGRLLLSRVQLHDSGNYSCTRAGRPGTGHLLVDVPPEPQLS	120		

QY	61	VLRPAAGSHPSRWAGMGRLLRLRSVQLHDHSGNYSCYRAGRPAQTVHLLVDVPPPEPQLS	120
Db	121	CFRKSPLSNVVCEWGPSPSTSLTKAVLLVRKFQNSPAEDFOEPCQYSOESOKFSQQLAV	180
QY	121	CFRKSPLSNVVCEWGPSPSTSLTKAVLLVRKFQNSPAEDFOEPCQYSOESOKFSQQLAV	180
Db	181	PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGILQDPPANITVTAVARNPRLSVTWQD	240
QY	181	PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGILQDPPANITVTAVARNPRLSVTWQD	240
Db	241	PHSNNSFYRLRFLRYRAERSKFTFTVMVKDLOHHCHVITHDAWSGLRHVVQLRAQEFGQ	300
QY	241	PHSNNSFYRLRFLRYRAERSKFTFTVMVKDLOHHCHVITHDAWSGLRHVVQLRAQEFGQ	300
Db	301	GEWSEWSPEAMGTPWTESRPPA	323
QY	301	GEWSEWSPEAMGTPWTESRPPA	323
RESULT	7		
ID		W70804; standard; protein; 360 AA.	
AC		W70804;	
DE		03-FEB-1999 (first entry)	
DT		Amino acid sequence of the interleukin (IL)-6R-alpha domain.	
KW		gp130; cytokine antagonist; interleukin; gamma-interferon;	
KW		granulocyte macrophage colony-stimulating factor; J peptide;	
KW		transforming growth factor-beta.	
OS		Synthetic.	
FH		Key	
FT		Location/Qualifiers	
FT		1..358	
FT		/note= "soluble interleukin (IL)-6R-alpha domain"	
FT		US5844099-A.	
PD		01-DEC-1998.	
PF		27-NOV-1995; 563105.	
PR		27-NOV-1995; US-563105.	
PR		20-OCT-1993; US-140222.	
PA		(REG-) REGENERON PHARM INC.	
PI		Economides A, Stahl N, Yancopoulos GD;	
PI		WPI; 99-044669/04.	
PT		Cytokine antagonists - comprising extracellular domains of	
PT		specificity-determining and signal-transducing components of	
PT		cytokine receptor	
PS		Example 4; Fig 15; 46pp; English.	
CC		The present sequence represents the amino acid sequence of interleukin	
CC		(IL)-6R-alpha domain. The protein is used in the course of the invention.	
CC		The specification describes cytokine antagonists comprising only the	
CC		extracellular domain of the specificity-determining component of	
CC		the cytokine receptor and the extracellular domain of a	
CC		signal-transducing component of the cytokine receptor. The cytokine	
CC		is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),	
CC		granulocyte macrophage colony-stimulating factor (GM-CSF),	
CC		gamma-interferon or transforming growth factor-beta (TGF-beta). The	
CC		antagonist is capable of binding the cytokine to form a nonfunctional	
CC		complex. The compounds have therapeutic activity as cytokine antagonists	
CC		and can also be used in assays for identifying novel agonists and	
CC		antagonists of cytokines.	
CSQ		Sequence 360 AA;	
Query Match		63.4%; Score 2391; DB 1; Length 360;	
Best Local Similarity		99.7%; Pred. No. 1.19e-184;	
Matches	322; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	

Query Match	63.4%;	Score 2391;	DB 1;	Length 360;
Best Local Similarity	99.7%;	Pred. No. 1.19e-184;		
Matches 322;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
dDb	1	MVAVCALLAALLAAPGAALAPRC	PAQEQVARGVLTSLPGDSVTLC	PCGVEPEDNATVHW 60
QY	1			
dDb	61	VLRPAAGSHPSRWAGMGRLLLSV	OLHDSGNSCYVRAGRPAGTVHLL	VDVPEEPQLS 120
QY	61	VLRPAAGSHPSRWAGMGRLLLSV	OLHDSGNSCYVRAGRPAGTVHLL	VDVPEEPQLS 120
dDb	121	CFRKSPISNVVCEWGPSTSLTTK	AVLLVRKFTQNSPAEDFQPCQY	SOBSQFSCQLAV 180
QY	121	CFRKSPISNVVCEWGPSTSLTTK	AVLLVRKFTQNSPAEDFQPCQY	SOBSQFSCQLAV 180


```

Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNPRLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNPRLSVTWQD 240
Db 241 PHSWNSFYRLRFLRYRAERSKFTFTMWKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
QY 241 PHSWNSFYRLRFLRYRAERSKFTFTMWKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
Db 301 GEWSEWSPEAMGTPWTESRPPA 323
QY 301 GEWSEWSPEAMGTPWTESRPPA 323

RESULT 8
ID R98364 standard; Protein; 468 AA.
AC R98364;
DE 28-NOV-1996 (first entry)
KW Interleukin-6; IL; receptor; antisense oligonucleotide; inhibition;
KW gene expression; kidney tumour; myeloma; Kaposi's sarcoma; psoriasis;
KW rheumatoid arthritis; endotoxic shock.
OS Homo sapiens.
PN W09618416-A1.
PD 20-JUN-1996.
PF 15-DEC-1995; J02587.
PR 16-DEC-1994; JP-313167.
PR 18-AUG-1995; JP-210739.
PA (CHUS) CHUGAI SEIYAKU KK.
PI Koishibara Y, Kuramaru K.
DR WPI; 96-300392/30.
DR N-PSDB; T31441.
PT Anti-sense oligo-nucleotide inhibitor against human IL-6R expression
PT - for treatment of e.g. tumours, cancers, rheumatoid arthritis,
PT psoriasis, endotoxic shock, etc.
PS Claim 2; Page 17-21; 32pp; Japanese.
CC Antisense oligonucleotides may be used to inhibit the expression of
CC the interleukin-6 receptor. Inhibition of expression of the
CC IL-6 receptor is useful in the treatment of kidney tumours, myeloma,
CC Kaposi's sarcoma, rheumatoid arthritis, psoriasis and endotoxic
CC shock. The antisense oligonucleotides are administered at a dosage
CC of 0.1-100mg/kg, pref. 0.1-50 mg/kg.
SQ Sequence 468 AA;

Query Match 63.4%; Score 2392; DB 1; Length 468;
Best Local Similarity 99.7%; Pred. No. 9,84e-185;
Matches 322; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLAVGCALLAALAAPCAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MLAVGCALLAALAAPCAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 61 LLRKPAGSHPSWAGMGRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
QY 61 LLRKPAGSHPSWAGMGRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
Db 121 CFRKSPLSNVVCEWGPSTPSLTATKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTATKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNPRLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNPRLSVTWQD 240
Db 241 PHSWNSFYRLRFLRYRAERSKFTFTMWKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
QY 241 PHSWNSFYRLRFLRYRAERSKFTFTMWKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
Db 301 GEWSEWSPEAMGTPWTESRPPA 323
QY 301 GEWSEWSPEAMGTPWTESRPPA 323

RESULT 9
ID P90525 standard; protein; 468 AA.
AC P90525;
DE 23-JAN-1990 (first entry)
KW B cell stimulating factor-2 receptor.
KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
OS Homo sapiens.
PN A08928720-A.
PD 27-JUL-1989.
PF 23-JAN-1989; 28720.
PR 22-JAN-1988; JP-012387.
PR 25-JAN-1988; JP-012599.
PR 04-AUG-1988; JP-194885.
PR 14-JAN-1989; JP-007461.
PA (KISH) Tadamitsu Kishimoto.
PI Kishimoto T;
DR WPI; 89-264012/37.
DR N-PSDB; P90525.
DE Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic and therapeutic agents for
PT associated disorders.
PS Claim 2; page 36; 76pp; english.
CC The BSF2 receptor is derived from a monocytic U937 cell line. It can be
CC used to develop prophylactic and therapeutic pharmaceuticals, as agents to
CC relate diseases and disorders to abnormal BSF-2 prodn. It can also be
CC used to study an immune mechanism with which BSF-2 or the receptor is
CC concerned.
SQ Sequence 468 AA;

Query Match 63.4%; Score 2390; DB 1; Length 468;
Best Local Similarity 99.7%; Pred. No. 1.45e-184;
Matches 322; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MLAVGCALLAALAAPCAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MLAVGCALLAALAAPCAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 61 VLKRPAGSHPSWAGMGRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
QY 61 VLKRPAGSHPSWAGMGRLLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
Db 121 CFRKSPLSNVVCEWGPSTPSLTATKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTATKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNPRLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVTAVARNPRLSVTWQD 240
Db 241 PHSWNSFYRLRFLRYRAERSKFTFTMWKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
QY 241 PHSWNSFYRLRFLRYRAERSKFTFTMWKDLQHHCVIHDANSGLRHVVQLRAQEEFGQ 300
Db 301 GEWSEWSPEAMGTPWTESRPPA 323
QY 301 GEWSEWSPEAMGTPWTESRPPA 323

RESULT 10
ID W70797 standard; protein; 592 AA.
AC W70797;
DE 03-FEB-1999 (first entry)
KW Human interleukin-6R-alpha-Pc.
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Protein 1..358
FT /note= "human IL-R-alpha"
FT Misc_difference 2
FT /label= L2V

```

FT Peptide /note= "changed to accomodate a Kozak sequence"
 FT 1. .19
 FT /note= "signal peptide"
 FT Misc_difference 359. .360
 FT /note= "Ala-Gly bridge"
 FT Protein 361. .552
 FT /note= "Fc domain of human IgG1"
 FT Disulfide_bond 371. .374
 PN US5844099-A.
 PD 01-DEC-1998.
 PF 27-NOV-1995; 563105.
 PR 27-NOV-1995; US-563105.
 PR 20-OCT-1993; US-140222.
 PA (REG-) REGENERON PHARM INC.
 PI Economides A, Stahl N, Yancopoulos GD;
 DR WPI; 99-044669/04.
 PR Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 PS Example 3; Fig 5; 46pp; English.
 CC The present sequence represents the amino acid sequence of human
 CC interleukin (IL)-6R-alpha-Fc. The protein is used in the course
 CC of the invention. The specification describes cytokine antagonists
 CC comprising only the extracellular domain of the specificity-determining
 CC component of the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC gamma-interferon or transforming growth factor (GM-CSF).
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 SQ Sequence 592 AA;

Query Match 63.4%; Score 2391; DB 1; Length 592;
 Best Local Similarity 99.7%; Pred. No. 1.19e-184;
 Matches 322; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MVAVCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPDNATVHW 60
 Qy 1 MLAVGCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPDNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Qy 1 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Db 121 CFRKSPLSNVVCEWGPRTSLTTPKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 Qy 121 CFRKSPLSNVVCEWGPRTSLTTPKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVTAVARNPRLSVTWQD 240
 Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVTAVARNPRLSVTWQD 240
 Db 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
 Qy 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
 Db 301 GEWSESPAMGTPWTESRSPPA 323
 Qy 301 GEWSESPAMGTPWTESRSPPA 323

RESULT 11
 ID W1371 standard; Protein; 468 AA.
 AC W1371;
 DT 02-FEB-1999 (first entry)
 DE Human interleukin-6 receptor alpha polypeptide.
 KW Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;
 SW therapy.
 OS Homo sapiens.
 PN WO9835694-A2.

PD 20-AUG-1998.
 PF 10-FEB-1998; U08898.
 PR 11-FEB-1997; US-795473.
 PA (DAVI/) DAVIDSON C M.
 DR (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 WPI; 98-520755/44.
 PT Treatment of hepatitis B virus infection - using a soluble active
 PT agent which prevents interaction of HBV with hepatocytes mediated by
 PT human interleukin 6
 PS Disclosure; Fig 9; 51pp; English.
 CC This is a previously reported amino acid sequence for human
 CC interleukin-6 (hIL-6) receptor alpha. The invention relates to
 CC the finding that hIL-6 is essential for hepatitis B virus (HBV)
 CC infection. The invention provides a pharmaceutical composition for
 CC the treatment of HBV infection, comprising a soluble active agent
 CC that interacts with at least one of the binding sites between hIL-6
 CC and the psi region of HBV and between hIL-6 and hepatocytes and
 CC other HBV-permissive cells. The active agent competitively binds
 CC to at least one of these sites and thereby prevents hIL-6-mediated
 CC HBV infection of hepatocytes and other HBV-permissive cells. The
 CC soluble active agent is selected from glycoprotein 80 (gp80) having
 CC receptor sites which interact with hIL-6, soluble glycoprotein 130
 CC (gp130) having receptor sites which interact with hIL-6, hIL-6
 CC derived peptide Lys41-Ala56, hIL-6 derived peptide Gly77-Glu95,
 CC hIL-6 derived peptide Gln153-His165, a combined 1 and 2 hIL-6
 CC mutant (mhIL-6 1+2), and mhIL-6 1+2 substituted with Phe171 to Leu
 CC and Ser177 to Arg, and mixtures of any of these.
 SQ Sequence 468 AA;

Query Match 62.9%; Score 2373; DB 1; Length 468;
 Best Local Similarity 99.1%; Pred. No. 3.83e-183;
 Matches 320; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Db 1 MLAVGCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPDNATVHW 60
 Qy 1 MLAVGCALLAALLAAGAAAPRRCPAQEVARGVLTSLPGDSVLTCPGVPEPDNATVHW 60
 Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAGTVHLLVDVPPPEPOLS 120
 Db 121 CFRKSPLSNVVCEWGPRTSLTTPKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 Qy 121 CFRKSPLSNVVCEWGPRTSLTTPKAVLLVRKFQNSPAEDFQPCQYQSQKFSQCLAV 180
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVTAVARNPRLSVTWQD 240
 Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQPDPPANITVTAVARNPRLSVTWQD 240
 Db 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
 Qy 241 PHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
 Db 301 GEWSESPAMGTPWTESRSPPA 323
 Qy 301 GEWSESPAMGTPWTESRSPPA 323

RESULT 12
 ID P50527 standard; protein; 323 AA.
 AC P50527;
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 KW B cell stimulating factor-2 receptor; monocyte U937 cell line.
 OS Homo sapiens.
 PN AU8928720-A.
 PD 27-JUL-1989.
 PF 23-JAN-1989; 28720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadimitsu Kishimoto.

PI Kishimoto T;
DR WPI: 89-264012/37.
DR N-P5DB; P90525.
PT Receptor protein for human B cell stimulating factor-2 - used for
PT developing prophylactic, therapeutic and diagnostic agents for
PT associated disorders.
PS Claim 6; page 39; 76pp; english.
CC The BSF2 receptor has amino acids at the C-terminal deleted. The receptor
CC is derived from a monocytic U937 cell line. It can be used to develop
CC prophylactic and therapeutic pharmaceuticals, as agents to relate
CC diseases and disorders to abnormal BSF-2 prodn. It can also be used to
CC study an immune mechanism with which BSF-2 or the receptor is concerned.
SQ Sequence 323 AA;

Query Match 62.3%; Score 2351; DB 1; Length 323;
Best Local Similarity 98.8%; Pred. No. 2.66e-181;
Matches 318; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Db 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120
QY 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDFQPCQYSQESQKFCOLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDFQPCQYSQESQKFCOLAV 180

Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240

Db 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300
QY 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300

Db 301 GGEWSESPAMGTPWTESRPP 322
QY 301 GGEWSESPAMGTPWTESRPP 322

RESULT 13
ID W70805 standard; protein; 315 AA.
AC W70805;
DT 03-FEB-1999 (first entry)
DE Amino acid sequence of the interleukin (IL)-6R-alpha-313 domain.
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
KW granulocyte macrophage colony-stimulating factor; J peptide;
KW transforming growth factor-beta.
OS Synthetic.
FH Key Location/Qualifiers
FT 1..313 /note= "truncated interleukin (IL)-6R-alpha domain"
FT US5844099-A.
PN 01-DEC-1998.
PD 27-NOV-1995; 563105.
PR 27-NOV-1995; US-563105.
PR 20-OCT-1993; US-140222.
PA (REG-) REGENERON PHARM INC.
PI Economides A, Stahl N, Yancopoulos GD;
DR WPI: 99-044669/04.
PT Cytokine antagonists - comprising extracellular domains of
PT specificity-determining and signal-transducing components of
PT cytokine receptor
PS Example 4; Fig 16; 46pp; English.
CC The present sequence represents the amino acid sequence of interleukin
CC (IL)-6R-alpha-313 domain. The protein is used in the course of the
CC invention. The specification describes cytokine antagonists comprising
CC only the extracellular domain of the specificity-determining component of
CC the cytokine receptor and the extracellular domain of a
CC signal-transducing component of the cytokine receptor. The cytokine

CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
CC granulocyte macrophage colony-stimulating factor (GM-CSF),
CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
CC antagonist is capable of binding the cytokine to form a nonfunctional
CC complex. The compounds have therapeutic activity as cytokine antagonists
CC and can also be used in assays for identifying novel agonists and
CC antagonists of cytokines.
SQ Sequence 315 AA;

Query Match 61.4%; Score 2317; DB 1; Length 315;
Best Local Similarity 99.7%; Pred. No. 1.86e-178;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 1 MIAVGCALLAALAPGAALAPRCAPAEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Db 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120
QY 61 VLKPPAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRAGTGHLLVDVPPPEPQLS 120

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDFQPCQYSQESQKFCOLAV 180
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLYRKFNQSPAEDFQPCQYSQESQKFCOLAV 180

Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240
QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFCGGLQDPDPANITVAVARNRWLSVTWQD 240

Db 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300
QY 241 PHSWNSFYRLRFELRYAERSKFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEFGQ 300

Db 301 GGEWSESPAMGT 313
QY 301 GGEWSESPAMGT 313

RESULT 14
ID R70122 standard; Protein; 1042 AA.
AC R70122;
DT 14-FEB-1996 (first entry)
DE IL8-R type 1-GBP 130 fusion protein.
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
KW red blood cell; cytokine receptor; glycophorin binding peptide 130;
KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
OS Chimeric Homo sapiens.
OS Chimeric Plasmodium falciparum.
FH Key Location/Qualifiers
FT misc_difference 54 /label= OTHER
FT W09506737-A.
PN 09-MAR-1995.
PD 01-SEP-1994; G01900.
PR 03-SEP-1993; GB-018350.
PR 23-AUG-1994; GB-017021.
PA (PREN/) PRENDERGAST K F.
PI Prendergast KF;
DR WPI: 95-115452/15.
PT New hybrid peptide(s) for binding cytokine(s) - comprising a
PT malaria parasite peptide capable of binding a red blood cell and
PT a receptor peptide.
PS Example A; Page 77-78; 93pp; English.
CC Hybrid peptides for binding cytokines, comprising a malaria parasite
CC (Plasmodium falciparum) peptide (capable of binding to a red blood
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
CC of these hybrid peptides. R70122 is a fusion of interleukin 6 receptor
CC (as confirmed with reference to SWISSPROT, as it is unclear in the
CC specification whether this sequence is IL6-R or IL8-R type) and
CC glycophorin binding protein (GBP) 130. The use of cytokine receptors not
CC normally found on RBCs means that the cytokine can bind harmlessly to the
CC RBC without deleterious effect. The RBC protects the hybrid peptides from

CC excretion from the kidney, and due to steric hindrance prevents the
 CC cytokines binding to a receptor in another cell. GBP 130 or GBPH
 CC (GBP homologue) are the prefid. malaria parasite peptides used, others
 CC include ERA 175 (175 kDa erythrocyte binding antigen), PMMSA (pre major
 CC merozoite surface antigen) and the Duffy binding receptor molecule (eg.
 CC exhibited by Plasmodium vivax). These peptides bind to pref. glycoprotein
 CC A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid
 CC peptides are thus used to lower the levels of free cytokines in the
 CC circulation to reduce pathological damage.
 SQ Sequence 1042 AA;

Query Match 56.0%; Score 2110; DB 1; Length 1042;
 Best Local Similarity 97.0%; Pred. No. 3.77e-161;
 Matches 295; Conservative 0; Mismatches 1; Indels 8; Gaps 2;
 Db 1 LAPRCRAQEVARGVLTSLPGDVTLLTCGVEPEDNATVHVLKRPAGSHPSXWAGMGR 60
 Qy 20 LAPRCRAQEVARGVLTSLPGDVTLLTCGVEPEDNATVHVLKRPAGSHPSXWAGMGR 79
 Db 61 RLLRSVLHDSGNYSY-AGRPAGTVHLLVDVPPPEPQLSCFRKPSLSNVVCEWGPST 119
 Qy 80 RLLRSVLHDSGNYSYRAGRAGTAVHLLVDVPPPEPQLSCFRKPSLSNVVCEWGPST 139
 Db 120 PSLTTKAVLLVRKFNQSPAEFQF-----SQKFSQCLAVPEGDSFFIIVSMCVASSVG 172
 Qy 140 PSLTTKAVLLVRKFNQSPAEFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQF 199
 Db 173 SKFSKTQFQCGGILQPPANNITVAVARNPRLSVTWQDPHNSWNSFYRLRFELRYRA 232
 Qy 200 SKFSKTQFQCGGILQPPANNITVAVARNPRLSVTWQDPHNSWNSFYRLRFELRYRA 259
 Db 233 ERSKTFTTMVKDLQHCVIHDAWSGLRHVQLRAQEEFGQGESEWSPAMGTPWTESR 292
 Qy 260 ERSKTFTTMVKDLQHCVIHDAWSGLRHVQLRAQEEFGQGESEWSPAMGTPWTESR 319
 Db 293 SPPA 296
 Qy 320 SPPA 323

RESULT 15
 ID P0526 standard; protein; 386 AA.
 AC P0526; 1990 (first entry)
 DT 25-JAN-1990 (first entry)
 DE B cell stimulating factor-2 receptor.
 KW B cell stimulating factor-2 receptor; monocytic U937 cell line.
 OS Homo sapiens.
 PN A08928720-A.
 PD 27-JUL-1989.
 PF 23-JAN-1989; 28720.
 PR 22-JAN-1988; JP-012387.
 PR 25-JAN-1988; JP-012599.
 PR 04-AUG-1988; JP-194885.
 PR 14-JAN-1989; JP-007461.
 PA (KISH) Tadamoto Kishimoto.
 PI Kishimoto T;
 DR WPI; 89-264012/37.
 DR N-PSDB; P90525.
 PT Receptor protein for human B cell stimulating factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for
 PT associated disorders
 PS Claim 4; page 37-8; 76pp; english.
 CC The BSF2 receptor has residues near the N-terminal deleted. The receptor
 CC is derived from a monocytic U937 cell line. It can be used to develop
 CC prophylactic and therapeutic pharmaceuticals as agents to relate diseases
 CC and disorders to abnormal BSF-2 prodn. It can also be used to study an
 CC immune mechanism with which BSF-2 or the receptor is concerned.
 SQ Sequence 386 AA;

Query Match 40.7%; Score 1534; DB 1; Length 386;
 Best Local Similarity 97.7%; Pred. No. 3.78e-113;
 Matches 211; Conservative 0; Mismatches 1; Indels 4; Gaps 2;

Db 28 VDVPPEPQLSCFRKPSLSNVVC--GPRSTPEWSITTKAVLLVRKFNQSPAEFQFQFQF 85
 Qy 110 VDVPPEPQLSCFRKPSLSNVVVCWGPSTP--SLTTKAVLLVRKFNQSPAEFQFQFQF 167
 Db 86 SQESQKFSQCLAVPEGDSFFIIVSMCVASSVGSFSTQTFQCGGILQPPANNITVAV 145
 Qy 168 SQESQKFSQCLAVPEGDSFFIIVSMCVASSVGSFSTQTFQCGGILQPPANNITVAV 227
 Db 146 ARNPRWLSVTWQDPHNSWNSFYRLRFELRYRAERSKTFTTMVKDLQHCVIHDAWSGLR 205
 Qy 228 ARNPRWLSVTWQDPHNSWNSFYRLRFELRYRAERSKTFTTMVKDLQHCVIHDAWSGLR 287
 Db 206 HVVOLRAQEEFGQGESEWSPAMGTPWTESRSPPA 241
 Qy 288 HVVOLRAQEEFGQGESEWSPAMGTPWTESRSPPA 323

Search completed: Thu Aug 10 16:13:25 2000
 Job time : 64 secs.

MSRCH_PP protein - protein database search, using Smith-Waterman algorithm

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Run on: Thu Aug 10 16:28:58 2000; MasPar time 19.54 Seconds
Tabular output not generated. 752.058 Million cell updates/sec

Title: >US-09-142-471-5
Description: (1-212) from US09142471.pep
Perfect Score: 1485
Sequence: 1 MNSFSTSAFGPVAFSLGILL.....LILSLKFLQSLRALRQM 212

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: sptrembl12

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 45.366; Variance 84.647; scale 0.536

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	1382	93.1	209	6	INTERLEUKIN-6 (FRAGMENT)	5.72e-273
2	940	63.3	209	6	INTERLEUKIN 6 (FRAGMENT)	5.49e-174
3	915	61.6	160	6	INTERLEUKIN-6 (FRAGMENT)	1.93e-168
4	892	60.1	208	6	INTERLEUKIN 6 PRECURSOR	2.41e-163
5	891	60.0	205	6	INTERLEUKIN 6 (FRAGMENT)	4.02e-163
6	855	57.6	207	6	INTERLEUKIN 6 (FRAGMENT)	3.68e-155
7	613	41.3	210	11	IL-6 (FRAGMENT)	3.42e-102
8	377	25.4	94	6	INTERLEUKIN 6 (FRAGMENT)	3.65e-52
9	320	21.5	101	11	INTERLEUKIN 6 (FRAGMENT)	1.51e-40
10	256	17.2	204	14	ORF K2	6.83e-28
11	256	17.2	204	14	INTERLEUKIN-6 HOMOLOG	6.83e-28
12	126	8.5	194	6	GRANULOCYTE COLONY-STI	1.03e-04
13	119	8.0	656	2	HYPOTHETICAL 74.9 KD P	1.20e-03
14	113	7.6	207	14	INTERLEUKIN-6 HOMOLOG	9.18e-03
15	113	7.6	214	11	GRANULOCYTE COLONY STI	9.18e-03
16	112	7.5	589	5	PF20 HOMOLOG	1.28e-02
17	109	7.3	219	13	PROGLUCAGON II	3.45e-02
18	109	7.3	321	10	SYNTAXIN-LIKE PROTEIN.	3.45e-02
19	107	7.2	251	2	O-ACETYL SERINE SYNTHAS	6.62e-02
20	106	7.1	266	13	PROGLUCAGON I.	9.15e-02

21	105	7.1	3027	4	Q9Y485	X-LIKE 1 PROTEIN.	1.26e-01
22	103	6.9	494	5	Q9X2W0	GABA-GATED CHLORIDE CH	2.38e-01
23	101	6.8	314	10	Q43864	ANNEXIN P35.	4.47e-01
24	101	6.8	815	10	Q22113	HCR2.	4.47e-01
25	99	6.7	195	6	O19180	GRANULOCYTE-COLONY STI	8.30e-01
26	100	6.7	298	10	Q43455	HEAT SHOCK TRANSCRIPTI	6.09e-01
27	100	6.7	496	5	O18468	GABA-GATED CHLORIDE CH	6.09e-01
28	99	6.7	780	11	Q60537	APOLIPOPROTEIN B (FRAG	8.30e-01
29	99	6.7	780	11	Q60536	APOLIPOPROTEIN (APOB)	8.30e-01
30	100	6.7	1099	10	Q9XK88	UNCONVENTIONAL MYOSIN	6.09e-01
31	99	6.7	1642	4	O14869	YOTIAO.	8.30e-01
32	100	6.7	1690	3	Q74835	PUTATIVE RRNA BIOGENES	6.09e-01
33	99	6.7	2500	5	O20937	SIMILAR TO S.	8.30e-01
34	99	6.7	3899	4	Q9Y6Y2	CENTROSOME-AND GOLGI-L	8.30e-01
35	99	6.7	3911	4	Q99996	HYPERION PROTEIN (YOTI	8.30e-01
36	96	6.5	241	14	Q04161	PHOSPHOPROTEIN (FRAGME	2.07e+00
37	97	6.5	373	4	Q9Y2X6	ARFAPTIN-1B.	1.53e+00
38	96	6.5	422	14	Q9WII5	GENE FOR THYMIDINE KIN	2.07e+00
39	96	6.5	759	14	Q67323	POLYMERASE.	2.07e+00
40	97	6.5	880	4	Q9Y4B0	P1.11659.3.	1.53e+00
41	96	6.5	1197	11	Q920R5	ESE2 PROTEIN.	2.07e+00
42	97	6.5	1419	5	Q45092	F58H7 6 PROTEIN.	1.53e+00
43	96	6.5	1658	11	Q920R6	ESE2L PROTEIN.	2.07e+00
44	97	6.5	1938	6	Q28641	MYOSIN HEAVY CHAIN.	1.53e+00
45	95	6.4	241	14	O42062	PHOSPHOPROTEIN.	2.79e+00

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	209 AA.
ID	Q9Y540			
AC	Q9Y540;			
DT	01-MAY-1999 (TrEMBLrel. 10, Created)			
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last annotation update)			
DE	INTERLEUKIN-6 (FRAGMENT).			
GN	IL-6.			
OS	Aotus nancyanae (Owl monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	ECHEVERRY S.J., HERNANDEZ E., MORENO A., PATARROYO M.E., MURILLO L.A.;			
RT	"Identification, cloning and sequencing of different interleukin genes			
RT	in 4 Aotus species."			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF014510; AAD01536.1; -			
DR	HSSP; P05231; IALU.			
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.			
FT	NON_TER 1			
FT	NON_TER 209			
SQ	SEQUENCE 209 AA; 23406 MW; 99D77053 CRC32;			

Query Match	93.1%	Score 1382;	DB 6;	Length 209;
Best Local Similarity	94.3%;	Pred. No. 5.72e-273;		
Matches	197;	Conservative	8;	Mismatches 43;
				Indels 0; Gaps 0;
Db	1	MNSFSTSAFGPVAFSLGILLVMPAAPPVPPGDSKSEVAAPNQPPLTSTEQIDKHIRYI	60	
QY	1	MNSFSTSAFGPVAFSLGILLVMPAAPPVPPGDSKSDVAAPHPQPLTSSERIDKQIRYI	60	
Db	61	LDGISALRKETCNKSNCESSKEALNNLNPMAKDCGCFQSGFNEETCLVKIITGLL	120	
QY	61	LDGISALRKETCNKSNCESSPEALANNLNPMAKDCGCFQSGFNEETCLVKIITGLL	120	
Db	121	EFVYLEYLQNRFSSESEQARAVQMSTKVLIOFLQKKAKNLDAITTPDPTTNASLLTKLQ	180	
QY	121	EFVYLEYLQNRFSSESEQARAVQMSTKVLIOFLQKKAKNLDAITTPDPTTNASLLTKLQ	180	
Db	181	AQNWLODMTHLILRSKFELQSLRAL	209	
QY	181	AQNWLODMTHLILRSKFELQSLRAL	209	

```

RESULT 2
ID Q28819 PRELIMINARY; PRT; 209 AA.
AC Q28819;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96163018.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,
RA STOTT J.L., FERRICK D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL; L46802; AAB01430.1; -.
DR HSSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 23483 MW; 29B594E3 CRC32;

Query Match 63.3%; Score 940; DB 6; Length 209;
Best Local Similarity 60.9%; Pred. No. 5.49e-174;
Matches 126; Conservative 39; Mismatches 42; Indels 0; Gaps 0;

Db 3 TSAFSPVAFSLGILLVMTAFPTPGVGSQADATSNRPPLTSPDKMEEFKIYLGKIS 62
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6 TSAFSPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYILDG 65
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 ALRKEMCKYKNCESKEALANNLKPKAEDKCGFSGFNOETCLFRITTTGLLEFQIH 122
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 ALRKETCNKSNCSPEALANNLKPMAEKDGCFOGSGFNEETCLVKIITGLLEFEVY 125
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 LKVIQIANTEGNKEDANSVYSTKLVLQMLKKVKSDQEVTTDPDTTSLQALKAQDKW 182
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 LEYLQNRFSSEEQARAVQMSKVLQIQLQKAKNLDAITTPDPTNASLLTKLQANQW 185
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
183 LKHTHTHLRLSLEDLFQFSRAVRIM 209
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
186 LEDMPHTHLRLSKLEFLQSLRALRQ 212
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
ID Q97535 PRELIMINARY; PRT; 160 AA.
AC Q97535;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Actus vociferans.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
RN [1]
RP SEQUENCE FROM N.A.
RA ECHEVERRY S.J., HERNANDEZ E., MORENO A., PATARROYO M.E., MURILLO L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
RT in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014505; AAD01531.1; -.
DR HSSP; P05231; 2IL6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
SQ SEQUENCE 160 AA; 17855 MW; EF6090C3 CRC32;

Query Match 61.6%; Score 915; DB 6; Length 160;
Best Local Similarity 59.5%; Pred. No. 2.41e-163;
Matches 122; Conservative 42; Mismatches 40; Indels 1; Gaps 1;

Db 2 NSLSTIAFSLGILLVMTAFPTPGPLGDFKDDTTSDDLTLTSPDKTALIKYILGKISA 61
QY :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 SAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYILDGISA 66
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 MRKEMCEKYDKCENSKALANNLKPMAEKDGCFOGSGFNOETCLMRITTTGLLEYQIYL 121
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 LRKETCNKSNCSPEALANNLKPMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYL 126
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 DYLQNEYEGDKGSIKALQILKQVKNPDEVTTTPDPTTNASLMNLSQNDW 181
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 EYLQNRFSSEEQARAVQMSKVLQIQLQKAKNLDAITTPDPTNASLLTKLQANQ-W 185
QY : : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 MRNTKIILRLSLENLFQFSRAVR 206
QY : : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
186 LEDMPHTHLRLSKLEFLQSLRALR 210
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
ID Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INTERLEUKIN 6 PRECURSOR.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Monodontidae;
OC Delphinapterus.
RN [1]
RP SEQUENCE FROM N.A.
RA ST-LAURENT G., DE GUISE S., FOURNIER M., ARCHAMBAULT D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AAD42929.1; -.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 0FA70646 CRC32;

Query Match 60.1%; Score 892; DB 6; Length 208;
Best Local Similarity 59.5%; Pred. No. 2.41e-163;
Matches 122; Conservative 42; Mismatches 40; Indels 1; Gaps 1;

Db 2 NSLSTIAFSLGILLVMTAFPTPGPLGDFKDDTTSDDLTLTSPDKTALIKYILGKISA 61
QY :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 SAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYILDGISA 66
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 MRKEMCEKYDKCENSKALANNLKPMAEKDGCFOGSGFNOETCLMRITTTGLLEYQIYL 121
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 LRKETCNKSNCSPEALANNLKPMAEKDGCFOGSGFNEETCLVKIITGLLEFEVYL 126
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 DYLQNEYEGDKGSIKALQILKQVKNPDEVTTTPDPTTNASLMNLSQNDW 181
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
127 EYLQNRFSSEEQARAVQMSKVLQIQLQKAKNLDAITTPDPTNASLLTKLQANQ-W 185
QY : : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 MRNTKIILRLSLENLFQFSRAVR 206
QY : : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
186 LEDMPHTHLRLSKLEFLQSLRALR 210
QY ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
ID Q28747 PRELIMINARY; PRT; 205 AA.
AC Q28747;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Orcinus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96163018.
RA KING D.P., SCHRENZEL M.D., MCKNIGHT M.L., REIDARSON T.H., HANNI K.D.,

```

Qy	125	YLEYLQNRFESSEQARAVQMSTKVLQFLOKKAKNLDATITPDPTTNASLLTKLQAQNO	184
Dd	180	WLKWTTHLIIRLEDLFQSLRAIRM	207
Qy	185	WLEDMPTHILIRSKEFLQRSRLALROM	212
RESULT	7		
ID	Q9WVQ8	PRELIMINARY;	PRT; 210 AA.
AC	Q9WVQ8;		
DT	01-NOV-1999	(TReMBRel. 12, Created)	
DT	01-NOV-1999	(TReMBRel. 12, Last sequence update)	
DT	01-NOV-1999	(TReMBRel. 12, Last annotation update)	
DE	IL-6	(FRAGMENT).	
OS	Mesocricetus auratus	(Golden hamster).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=APA; TISSUE=KIDNEY;		
RA	NISHIDA E.;		
RT	"APA hamsters IL-6 partial cDNA."		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AB028635; BAA78766.1; -.		
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.		
FT	NON_TER	1	
SQ	SEQUENCE	210 AA; 24060 MW; 0307F113 CRC32;	
Query Match	41.3%;	Score 613;	DB 11; Length 210;
Best Local Similarity	39.5%;	Pred. No. 3.42e-102;	
Matches	83;	Conservative 58; Mismatches 65;	Indels 4; Gaps
Dd	2	LSARDFHLPV-LGILLVMATALPTSQVRGDFTD-TTPNRPVYTTSQQVGGLVTYVLR	59
Qy	4	FSTAAGFAVESGLLVLPAPFPAP-VPGEDSKOVAAPHROPLTSERIDKQIRYLD	62
Dd	60	EIYELRCLNNPCGMNDYVLENNDELFPVTOINDGCLQTGYNWICLLKITSGLLDY	119
Qy	63	GISALRKETCNKNCESSPEALAEENLNPKMAEKDCFCQSGNETCLVKIITGLFE	122
Dd	120	QIYLEFTVNVDNKDKARVIQSITIKLSQIFQEYKVGPKIVTSPSPSKAILMEKLES	179
Qy	123	EVLYEYLQNRP-ESSEQARAVQMSTKVLQFLOKKAKNLDATITPDPTTNASLLTKLA	181
Dd	180	QKWPRTKTIKLILKAEEFLEVMTMRSTQ	209
Qy	182	QNMLEDMPHILRSKEFLQRSRLALRQ	211
RESULT	8		
ID	O62775	PRELIMINARY;	PRT; 94 AA.
AC	O62775;		
DT	01-AUG-1998	(TReMBRel. 07, Created)	
DT	01-AUG-1998	(TReMBRel. 07, Last sequence update)	
DT	01-NOV-1999	(TReMBRel. 12, Last annotation update)	
DE	INTERLEUKIN 6	(FRAGMENT).	
OS	Felis silvestris catus	(Cat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	HARLEY R., HELPS C.R., GRUFFYDD-JONES T.J., DAY M.J., HARBOUR D.A.;		
RL	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF054603; AAC15976.1; -.		
DR	HSSP; P05231; 2IL6.		
DR	PFAM; PF00489; IL-6; 1.		
FT	NON_TER	1	
SQ	SEQUENCE	94 AA; 11099 MW; 835867E6 CRC32;	
Query Match	25.4%;	Score 377;	DB 6; Length 94;
Best Local Similarity	48.9%;	Pred. No. 3.65e-52;	
Matches	46;	Conservative 21; Mismatches 27;	Indels 0; Gaps

Db 64 CHHSTLCRVREYPRIMSFVHFPIILMSNVECORREFRGAECMNAMVRLRAYESYLTRLM 123

QY 72 CKNSNCESSPALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLEYLQN 131
Db 124 LLDDAPGDADAAAGSANTVVLVSALDSLIEELPVNNKKGGAESNEKTVRALGGQSPRDVV 183
QY 132 REF-SS-EQARAVOMSTKVLIQFLQKKAKNLDATT-PDPTTNASLLTKLQAQNWLED 188

Db 184 LSAFRILEYQLMFLRDGRRAIAMM 207
QY 189 MPHTLILRSKREFLQSLRALRQM 212

RESULT 15
ID P97712 PRELIMINARY; PRT; 214 AA.
AC P97712;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE GRANULOCYTE COLONY STIMULATING FACTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97074656.
RA HAN S.W., RAMESH N., OSBORNE W.R.A.;
RT "Cloning and expression of the cDNA encoding rat granulocyte colony-
stimulating factor";
RL Gene 175:101-104(1996).
DR EMBL; U37101; AAC52915.1; -.
DR HSSP; P09919; IRHG.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PFAM; PF00489; IL-6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
SQ SEQUENCE 214 AA; 23659 MW; F2592D0C CRC32;

Query Match 7.6%; Score 113; DB 11; Length 214;
Best Local Similarity 21.0%; Pred. No. 9.18e-03;
Matches 33; Conservative 40; Mismatches 79; Indels 5; Gaps 5;
Db 47 QVRKIQARNTLEQLCATYKLCHPPELVLFHSGHIGIPK-ASLSSCSQALQOTKCLSQL 105
QY 56 QIRYLDGISALRKETCNKSNCESSPEALAEENNLNPKMAEKDGCQSGFNEETCLVKI 115
Db 106 HSGFLYQGLLQALAG-I-SSE-LAPTIDMLHLDVDFATTIWOQMESLGA-PTVOPTQ 161
QY 116 ITGLLEFEVLEYLQNRFESESEQARAVOMSTKVLIQFLQKKAKNLDATTDPPTNASL 175
Db 162 STMPIFTSAFORRAGGVLVTSYLOSFLETAHHL 198
QY 176 LTKLQAQNWLEDMPHTLILRSKREFLQSLRALRQM 212

Search completed: Thu Aug 10 16:30:56 2000
Job time : 118 secs.

(MT)

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match						
1	1446	97.4	212	1	IL6_HUMAN		INTERLEUKIN-6 PRECURSOR	5.60e-29
2	1410	94.9	212	1	IL6_MACMU		INTERLEUKIN-6 PRECURSOR	1.45e-28
3	1403	94.5	212	1	IL6_CERTO		INTERLEUKIN-6 PRECURSOR	6.25e-28
4	1402	94.4	212	1	IL6_MACP		INTERLEUKIN-6 PRECURSOR	1.07e-28
5	953	64.2	212	1	IL6_PIG		INTERLEUKIN-6 PRECURSOR	1.50e-18
6	940	63.3	209	1	IL6_PHOVI		INTERLEUKIN-6 PRECURSOR	1.46e-17
7	939	63.2	208	1	IL6_HORSE		INTERLEUKIN-6 PRECURSOR	2.47e-17
8	891	60.0	205	1	IL6_ORCOR		INTERLEUKIN-6 PRECURSOR	2.54e-16
9	891	60.0	208	1	IL6_FELCA		INTERLEUKIN-6 PRECURSOR	2.54e-16
10	875	58.9	207	1	IL6_CANCA		INTERLEUKIN-6 PRECURSOR	1.17e-16
11	807	54.3	208	1	IL6_CAPHI		INTERLEUKIN-6 PRECURSOR	3.94e-14
12	804	54.1	208	1	IL6_SHEBP		INTERLEUKIN-6 PRECURSOR	1.90e-14
13	804	54.1	208	1	IL6_BOVIN		INTERLEUKIN-6 PRECURSOR	1.90e-14
14	710	47.8	207	1	IL6_MARMO		INTERLEUKIN-6 PRECURSOR	4.04e-12
15	650	43.8	211	1	IL6_MOUSE		INTERLEUKIN-6 PRECURSOR	1.33e-11
16	642	43.2	211	1	IL6_RAT		INTERLEUKIN-6 PRECURSOR	8.29e-11
17	490	33.0	125	1	IL6_MUSVI		INTERLEUKIN-6 (11-6) (4.50e-78
18	166	11.2	201	1	MGF_CHICK		MYELOMONOCYTIC GROWTH	1.20e-11
19	126	8.5	194	1	CSF3_CANCA		GRANULOCYTE COLONY-STI	5.78e-05
20	116	7.8	175	1	CSF3_FELCA		GRANULOCYTE COLONY-STI	1.94e-03
21	108	7.3	208	1	CSF3_MOUSE		GRANULOCYTE COLONY-STI	2.85e-02
22	103	7.3	1102	1	MYSC_CHICK		MYOSIN HEAVY CHAIN, CA	2.05e-02
23	103	6.9	454	1	MSRE_RABIT		MACROPHAGE SCAVENGER R	1.43e-01

RX MEDLINE; 88088768.
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.,
RT "Molecular cloning and expression of hybridoma growth factor in
RT Escherichia coli";
RL J. Immunol. 139:4116-4121(1987).
RN [16]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89391958.
RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
RT stabilization of the mRNA and high-level expression in mouse NIH3T3
RT cells";
RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89391958.
RA Tissue=FIBROBLAST;
RX MEDLINE; 87004683.
RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
RA Fiers W.;
RT "Structural analysis of the sequence coding for an inducible 26-kDa
RT protein in human fibroblasts";
RL Eur. J. Biochem. 159:625-632(1986).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89193317.
RA Wong G., Witke-Giannotti J., Hewick R., Clark S., Ogawa M.;
RT "Interleukin 6: Identification as a hematopoietic colony-stimulating
RT factor";
RL Behring Inst. Mitt. 83:40-47(1988).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93178270.
RA Chen Q.Y.;
RT "Stable and efficient expression of human interleukin-6 cDNA in
RT mammalian cells after gene transfer";
RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
RN [10]
RP SEQUENCE OF 30-63.
RX MEDLINE; 88154445.
RA Van Damme J., van Beunnen J., Decock B., van Snick J., de Ley M.,
RA Billiau A.;
RT "Separation and comparison of two monokines with
RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
RT factor (HGF). Identification of leukocyte-derived HGF as IL-6";
RL J. Immunol. 140:1534-1541(1988).
RN [11]
RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
RX MEDLINE; 95154344.
RA Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
RA Ziliotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
RT "Structure, stability and biological properties of a N-terminally
RT truncated form of recombinant human interleukin-6 containing a single
RT disulfide bond";
RL Eur. J. Biochem. 227:573-581(1995).
RN [12]
RP DISULFIDE BONDS.
RX MEDLINE; 89286115.
RA Clouston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RT "Disulfide structures of human interleukin-6 are similar to those of
RT human granulocyte colony stimulating factor";
RL Arch. Biochem. Biophys. 272:144-151(1989).
RN [13]
RP MUTAGENESIS.
RX MEDLINE; 91243808.
RA Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an
RT alpha-helical structure of the C-terminus for biological activity of
RT human IL-6";
RL FEBS Lett. 282:265-267(1991).
RN [14]
RP STRUCTURE BY NMR.
RX MEDLINE; 96134845.

RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
RT by NMR spectroscopy";
RL Biochemistry 35:273-281(1996).
RN [15]
RP STRUCTURE BY NMR.
RX MEDLINE; 97303053.
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6";
RL J. Mol. Biol. 268:468-481(1997).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE; 97224126.
RA Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling";
RL EMBO J. 16:989-997(1997).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04430; CAA28026.1; -
DR EMBL; M14584; AAA52728.1; -
DR EMBL; X04602; CAA28268.1; -
DR EMBL; Y00081; CAA68278.1; -
DR EMBL; M18403; AAA52729.1; -
DR EMBL; M29150; AAA59154.1; -
DR EMBL; X04402; CAA27990.1; -
DR EMBL; X04403; CAA27991.1; -
DR EMBL; M54894; AAC41704.1; -
DR EMBL; S56892; AAD13886.1; -
DR EMBL; A09363; CAA00839.1; -
DR PIR; A32648; IVHUB2.
DR PIR; A25921; A25921.
DR PDB; 1IL6; 04-FEB-98.
DR PDB; 2IL6; 04-FEB-98.
DR PDB; 1ALU; 03-JUN-98.
DR MIM; 147620; -
DR PFAM; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFPGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT MUTAGEN 173 173 A->V: ALMOST NO LOSS OF ACTIVITY.
FT MUTAGEN 185 185 W->R: NO LOSS OF ACTIVITY.
FT MUTAGEN 204 204 S->P: 13% ACTIVITY.
FT MUTAGEN 210 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
SQ SEQUENCE 212 AA; 23718 MW; 1FIEDIFE1B734079 CRC64;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 5 60e-297;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 1 MNSFTSAFGPVAFSLGLLLVLPAAFPAPVPPGDSKDVAAAPHROPPLTSSERIKOIRY 60
|||||

QY 1 MNSFSTAFGVPFVSLGILLVLPAAFPAPVPPGDSKDVAAAPHQRPITSSERIDKHRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 Db 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLIQFLQKAKNLDATITPDPPTNASLLTKLQ 180
 QY 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLIQFLQKAKNLDATITPDPPTNASLLTKLQ 180
 Db 181 AQONWLODMTHILRSKFELQSLRALROM 212
 QY 181 AQONWLODMTHILRSKFELQSLRALROM 212

RESULT 2
 ID IL6_MACMU STANDARD; PRT; 212 AA.
 AC P51494;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RAC 2;
 RX MEDLINE; 96003435.
 RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L26028; AAA99978.1; -.
 CC DR HSSP; P05231; 1ALU.
 CC DR PFAM; PR00489; IL6; 1.
 CC DR PRINTS; PR00433; IL6GSGFMGF.
 CC DR PRINTS; PR00434; INTERLEUKIN6.
 CC DR PROSITE; PS00254; INTERLEUKIN6; 1.
 CC KW Cytokine; Glycoprotein; Growth factor; Signal.
 CC FT SIGNAL 1 29 BY SIMILARITY.
 CC FT CHAIN 30 212 INTERLEUKIN-6.
 CC FT DISULFID 72 78 POTENTIAL.
 CC FT DISULFID 101 111 POTENTIAL.
 CC FT CARBOHYD 73 73 POTENTIAL.
 CC FT CARBOHYD 172 172 POTENTIAL.
 CC SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCAD CRC64;

Query Match 94.9%; Score 1410; DB 1; Length 212;
 Best Local Similarity 93.9%; Pred. No. 1.45e-288;
 Matches 199; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Db 1 MNSFSTAFGVPFVSLGILLVLPAAFPAPVPPGDSKDVAAAPHQRPITSSERIDKHRYI 60
 QY 1 MNSFSTAFGVPFVSLGILLVLPAAFPAPVPPGDSKDVAAAPHQRPITSSERIDKHRYI 60

Db 61 LDGIALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120
 Db 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLIQFLQKAKNLDATITPDPPTNASLLTKLQ 180
 QY 121 EFVYLEYLQNRFFESSEBQARAVQMSKVLIQFLQKAKNLDATITPDPPTNASLLTKLQ 180
 Db 181 AQONWLODMTHILRSKFELQSLRALROM 212
 QY 181 AQONWLODMTHILRSKFELQSLRALROM 212

RESULT 3
 ID IL6_CERTO STANDARD; PRT; 212 AA.
 AC P46550;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Carcocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Cercocebus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FUJ;
 RX MEDLINE; 96003435.
 RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L26032; AAA99972.1; -.
 CC DR HSSP; P05231; 1ALU.
 CC DR PFAM; PR00489; IL6; 1.
 CC DR PRINTS; PR00433; IL6GSGFMGF.
 CC DR PRINTS; PR00434; INTERLEUKIN6.
 CC DR PROSITE; PS00254; INTERLEUKIN6; 1.
 CC KW Cytokine; Glycoprotein; Growth factor; Signal.
 CC FT SIGNAL 1 29 BY SIMILARITY.
 CC FT CHAIN 30 212 INTERLEUKIN-6.
 CC FT DISULFID 72 78 POTENTIAL.
 CC FT DISULFID 101 111 POTENTIAL.
 CC FT CARBOHYD 73 73 POTENTIAL.
 CC FT CARBOHYD 172 172 POTENTIAL.
 CC SQ SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match 94.5%; Score 1403; DB 1; Length 212;
 Best Local Similarity 93.4%; Pred. No. 6.25e-287;
 Matches 198; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Db 1 MNSFSTAFGVPFVSLGILLVLPAAFPAPVPPGDSKDVAAAPHQRPITSSERIDKHRYI 60
 QY 1 MNSFSTAFGVPFVSLGILLVLPAAFPAPVPPGDSKDVAAAPHQRPITSSERIDKHRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFOGSGNEETCLVKIITGLL 120

QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCFCQSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFFESSEQARAVOMSTKVLIQLOKAKNLDATTPEPTNASLLTKLQ 180

QY 121 EFVYLEYLQNRFFESSEQARAVOMSTKVLIQLOKAKNLDATTPEPTNASLLTKLQ 180

Db 181 AQONWLODMTHILRSFKFLOSSLRALROM 212

QY 181 AQONWLODMTHILRSFKFLOSSLRALROM 212

RESULT 4

ID IL6_MACFA STANDARD; PRT; 212 AA.

AC P79341;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

GN IL6.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheinae; Macaca.

RN [1]

RP SEQUENCE FROM N.A.

RA Tatsumi M.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND

CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AB000554; BAA19148.1; -

DR HSSP; P05231; 2IL6.

DR PFAM; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR PROSITE; PR00434; INTERLEUKIN_6.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 29 BY SIMILARITY.

FT CHAIN 30 212 INTERLEUKIN-6.

FT DISULFID 72 78 POTENTIAL.

FT DISULFID 101 111 POTENTIAL.

FT CARBOHYD 73 73 POTENTIAL.

FT CARBOHYD 172 172 POTENTIAL.

SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF080389 CRC64;

Query Match 94.4%; Score 1402; DB 1; Length 212;

Best Local Similarity 94.3%; Pred. No. 1.07e-286;

Matches 200; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 1 MNSVSTAFGVPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHRYI 60

QY 1 MNSVSTAFGVPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHRYI 60

Db 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCFCQSGFNEETCLVKIITGLL 120

QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCFCQSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFFESSEQARAVOMSTKVLIQLOKAKNLDATTPEPTNASLLTKLQ 180

QY 121 EFVYLEYLQNRFFESSEQARAVOMSTKVLIQLOKAKNLDATTPEPTNASLLTKLQ 180

Db 181 AQONWLODMTHILRSFKFLOSSLRALROM 212

QY 181 AQONWLODMTHILRSFKFLOSSLRALROM 212

RESULT 5

ID IL6_PIG STANDARD; PRT; 212 AA.

AC P26893;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

GN IL6.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

RN [1]

RP SEQUENCE FROM N.A.

RX Richards C., Saklatvala J.;

RA "Molecular cloning and sequence of porcine interleukin 6 cDNA and

RT expression of mRNA in synovial fibroblasts in vitro.";

RL Cytokine 3:269-276(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX Mathialagan N., Bixby J.A., Roberts M.R.;

RA "Expression of Interleukin-6 in porcine, ovine, and bovine

RT preimplantation conceptuses.";

RL Mol. Reprod. Dev. 32:324-330(1992).

CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND

CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M86722; AAC37333.1; -

DR EMBL; M80258; AAC27127.1; -

DR HSSP; P05231; IL6.

DR PFAM; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR PROSITE; PR00434; INTERLEUKIN_6.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 29 BY SIMILARITY.

FT CHAIN 30 212 INTERLEUKIN-6.

FT DISULFID 72 78 BY SIMILARITY.

FT DISULFID 101 111 BY SIMILARITY.

FT CONFLICT 30 30 G -> E (IN REF. 2).

SQ SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match 64.2%; Score 953; DB 1; Length 212;

Best Local Similarity 61.3%; Pred. No. 1.50e-182;

Matches 130; Conservative 42; Mismatches 40; Indels 0; Gaps 0;

Db 1 MNSVSTAFGVPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHRYI 60

QY 1 MNSVSTAFGVPVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHQPLTSSERIDKHRYI 60

Db 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCFCQSGFNEETCLVKIITGLL 120

QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNPMAEKDGCFCQSGFNEETCLVKIITGLL 120

Db 121 EFQIYLDYLOKEYESKNGVNEAVQISTKALIQTLROKGNPKDKATPTNPTNAGLLDKLQ 180

DB 183 LKHTTTHLILKRSLEDFLQFSLRAVRIM 209

.....

Db 58 LGKISALKNEMCNFNSKSCENSKEVLAENNLLPKMAEKDGCFSQSGFNQETCLMKITTGLS 117

QY 61 LOGISALRKTCKNSMCESSPEALANNLNLPKMAEKDCQSGFNEETCLVKIITGLL 120
 Db 118 EFOIYLEYLQNEFKGKBNKIMQISTKVLVOILMOKKNPE-VTTPDPTAKSLAKLH 176
 QY 121 EREVLEYLQNEFSEGEQARVQSTKVLIQFKKAKNLDAITTPDPTNASLTLKQ 180
 Db 177 SQNEWLKNTTTHILRSLEDFLQSLRAVRIM 208
 QY 181 AQOWLEDMPTHLILRSLEFLQSLRALRQM 212

RESULT 8
 ID IL6_ORCOR STANDARD; PRT; 205 AA.
 AC Q28747;
 DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DE 15-FEB-2000 (Rel. 39, Last annotation update)
 GN INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 OS Orcinus orca (Killer whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Orcinus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96163018.
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Stott J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RL Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 CC EMBL; L45803; AB01429.1; -;
 CC HSSP; P05231; IALU.
 CC DR PFAM; PF00489; IL6; 1.
 CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 CC KW Cytokine; Glycoprotein; Growth factor; Signal.
 CC FT NON_TER 1 1
 CC FT SIGNAL <1 21 BY SIMILARITY.
 CC FT CHAIN 22 205 INTERLEUKIN-6.
 CC FT DISULFID 64 70 BY SIMILARITY.
 CC FT DISULFID 93 103 BY SIMILARITY.
 CC FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;

Query Match 60.0%; Score 891; DB 1; Length 205;
 Best Local Similarity 61.8%; Pred. No. 2.54e-168;
 Matches 123; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
 Db 5 AFSGLLLVYATAPPTGPGIPEGDFKDDTTSDRLYLISPDKTEALIKYILGKISAMKEMC 64
 QY 13 AFSGLLLVLPAPAPVPPGDSKDVAAPHROPLTSSERIDKQIRYILGISALRKTC 72
 Db 65 EKYDKNSKEALANNLNLPKMAEKDCQSGFNOETCLMRITTGLEYQIYLDYLONE 124
 QY 73 NKSNCWESSPEALANNLNLPKMAEKDCQSGFNEETCLVKIITGLLEFVLEYLQNR 132

Db 125 YEGDKEATEAVQISSKALAQILROKVKNPDEVTPDPTTNASLMNNLOSQNDWMKNTKI 184
 QY 133 FESSEQARAVQSTKVLIQFKKAKNLDAITTPDPTNASLTLKQAOQO-WLEDMP 191
 Db 185 ILILRSLEFLQSLRAIR 203
 QY 192 HLILRSLEFLQSLRALR 210

RESULT 9
 ID IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 GN INTERLEUKIN-6 PRECURSOR (IL-6).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94162386.
 RA Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
 RA Hasegawa A.;
 RT "Molecular cloning of feline interleukin-6 cDNA";
 RL J. Vet. Med. Sci. 55:941-944(1993).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC TISSUE-LYMPHOCYTES;
 CC RX MEDLINE; 94052249.
 CC RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
 CC RT "Molecular cloning and characterization of a cDNA encoding feline
 CC interleukin-6";
 CC Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
 CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL; L16914; AAA16620.1; -;
 CC DR EMBL; D13227; BAA02507.1; -;
 CC DR HSSP; P05231; 2IL6.
 CC DR PFAM; PF00489; IL6; 1.
 CC DR PRINTS; PR00433; IL6GCSFMGF.
 CC DR PRINTS; PR00434; INTERLEUKIN_6.
 CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 CC KW Cytokine; Glycoprotein; Growth factor; Signal.
 CC FT SIGNAL 1 27 POTENTIAL.
 CC FT CHAIN 28 208 INTERLEUKIN-6.
 CC FT DISULFID 68 74 BY SIMILARITY.
 CC FT DISULFID 97 107 BY SIMILARITY.
 CC FT CONFLICT 2 2 T -> N (IN REF. 2).
 CC FT CONFLICT 45 45 S -> P (IN REF. 2).
 CC FT CONFLICT 133 133 E -> K (IN REF. 2).
 CC FT CONFLICT 173 187 AKLQSQEELWRLHTTI -> LSCSHRRVAAEHNH (IN
 CC REF. 2).
 CC FT CONFLICT 200 201 FS -> LR (IN REF. 2).
 CC SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

Query Match 60.0%; Score 891; DB 1; Length 208;
 Best Local Similarity 57.5%; Pred. No. 2.54e-168;

Qy	7	SAGFPVAFSLGLLVLPAAFPAPVPVPGEDSKDVAAPIHQPLTSSERIDKQIRYILDGISA	66
Db	62	LRKEMCDKFNKCKEDSKALAEENLHLPKLEGKDCQFSGFNOETCLTRITTTGLVFEQOLHL	121
Qy	67	LRKCTNCKSNKCESSPEALAEENLNLPKMAEKDCQFSGFNEETCLVKITGLLEFEVL	126
Db	122	NILQNNYEGDKENKSVHMTSKILVOMLSKVKNQDEVTPPTDASLOALQSODECV	181
Qy	127	EYLQNPRESSSEQARAVOMSTKVLQFLQKAKNLDAITTPDPTNASTLLTKLQAQOWL	186
Db	182	KHTIHLILRSLEDFLQFSLRVRIM	207
Qy	187	EDMPHTHLILRSLEDFLQFSLRVRIM	212
RESULT 11			
ID	IL6_CAPHI	STANDARD;	PRT; 208 AA.
AC	Q28319;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DE	15-JUL-1998 (Rel. 36, Last annotation update)		
DE	INTERLEUKIN-6 PRECURSOR (IL-6).		
GN	IL6.		
OS	Capra hircus (Goat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Caprinae; Capra.		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE; 97392354.		
RT	Takakura H., Mori Y., Tatsumi M.;		
RT	"Molecular cloning of caprine IL-6 cDNA and its expression in insect		
RT	cells.";		
CC	Int. Arch. Allergy Immunol. 113:409-416(1997).		
CC	-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL		
CC	OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND		
CC	PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN		
CC	HAPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.		
CC	-1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collabor		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstat		
CC	the European Bioinformatics Institute. There are no restrictions on		
CC	use by non-profit institutions as long as its content is in no		
CC	modified and this statement is not removed. Usage by and for comm		
CC	entities requires a license agreement (See http://www.isb-sib.ch/anno		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; D86569; BAA13118.1; -		
DR	HSSP; P05231; 21L6.		
DR	PFAM; PF00489; IL6; 1.		
DR	PRINTS; PR00433; IL6GCSFMGF.		
DR	PRINTS; PR00434; INTERLEUKIN_6.		
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.		
KW	Cytokine; Glycoprotein; Growth factor; Signal.		
FT	SIGNAL 1 29		
FT	CHAIN 30 208		
FT	DISULFID 72 78		
FT	DISULFID 101 111		
FT	CARBOHYD 38 38		
FT	POTENTIAL.		
Qy	SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;		
Query Match 54.38; Score 807; DB 1; Length 208;			
Best Local Similarity 53.38; Pred. No. 3.94e-149;			
Matches 112; Conservative 48; Mismatches 46; Indels 4; Gaps			
Db	1	MNSLFTSAFSLAVSLGLLVMTSAFPTGPLEGDKNDTPSRLLLTTPKTEALIKHI	60
Qy	1	MNSESTSAFGVAFSLGLLVLPAAFPAPVPVPGEDSKDVAAPIHQPLTSSERIDKQIRY	60
Db	61	VDKISAIRICEKNCENSKETLAENKLUKLPKMEKDCGCFSGNQALCIKTTAGLL	120

QY 61 LDG1SALRKETCNKSNMCSSPEALANNLNPMAEKDGCFCQSGFNEETCLVKIITGLL 120
 Db 121 EYQIYLDLQNEFEQNOETVMELOSSIRTLQIOLKEKIAGL--ITTP--ATNMDLMEKMQ 176
 QY 121 EFEVLEYLQNEFESEEQARAVQMTKVLQFLOKAKNLDAITPDPDTNASLTLKLQ 180
 Db 177 SNEWKNAKVIIILRSLENFLQFSRLAIR 206
 QY 181 AQONWLEDMPTHLILRSLEKFLQSLRALR 210
 RESULT 12
 ID IL6_SHEEP STANDARD; PRT; 208 AA.
 AC P29455;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94041419.
 RA Andrews A.E., Barcham G.J., Ashman K., Meeusen E.N.T., Brandon M.R.,
 RA Nash A.D.;
 RT "Molecular cloning and characterization of a ruminant interleukin-6
 RT cDNA.";
 RL Immunol. Cell Biol. 71:341-348(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ebrahim B.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS IN THE FINAL DIFFERENTIATION
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X62501; CAA44363.1; -;
 DR EMBL; X68723; CAA48662.1; -;
 DR EMBL; A19159; CAA01443.1; -;
 DR PIR; S29549; S29549.
 DR HSSP; P05231; 2IL6.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCFMGF.
 DR PROSITE; PR00434; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 208
 FT BY SIMILARITY.
 FT INTERLEUKIN-6.
 FT DISULFID 72 78
 FT BY SIMILARITY.
 FT CARBOHYD 38 38
 FT BY SIMILARITY.
 FT CONFLICT 4 4
 FT L -> R (IN REF. 2).
 FT CONFLICT 110 110
 FT I -> V (IN REF. 2).
 FT CONFLICT 171 171
 FT M -> L (IN REF. 2).
 FT CONFLICT 201 201
 FT S -> R (IN REF. 2).
 SQ SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;
 Query Match 54.1%; Score 804; DB 1; Length:208;
 Best Local Similarity 52.9%; Pred. No. 1.90e-148;
 Matches 112; Conservative 48; Mismatches 46; Indels 4; Gaps 2;

Matches 111; Conservative 49; Mismatches 46; Indels 4; Gaps 2;
 Db 1 MNSLTSAPSLAVSLGILLVMTSAFPTGPGLEDGFKNDTPSRLLLTTPKTEALIKRI 60
 QY 1 MNSFSTSAFPGVAFSLGILLVLPAAFPAPVPFGEDSKDVAAPHRQPLTSSERIDQIRYI 60
 Db 61 VDKISAIRKEICEKNDCEKSETLAENKLLPKMEEKDGCFCQSGFNAICLIKTAGLL 120
 QY 61 LDG1SALRKETCNKSNMCSSPEALANNLNPMAEKDGCFCQSGFNEETCLVKIITGLL 120
 Db 121 EYQIYLDLQNEFEQNOETVMELOSSIRTLQIOLKEKIAGL--ITTP--ATNMDLMEKMQ 176
 QY 121 EFEVLEYLQNEFESEEQARAVQMTKVLQFLOKAKNLDAITPDPDTNASLTLKLQ 180
 Db 177 SNEWKNAKVIIILRSLENFLQFSRLAIR 206
 QY 181 AQONWLEDMPTHLILRSLEKFLQSLRALR 210
 RESULT 13
 ID IL6_BOVIN STANDARD; PRT; 208 AA.
 AC P26892;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HOLSTEIN;
 RX MEDLINE; 93076003.
 RA Drogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
 RT "Nucleotide sequence of bovine interleukin-6 cDNA.";
 RL DNA Seq. 2:411-413(1992).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X57317; CAA40572.1; -;
 DR PIR; S22162; S22162.
 DR HSSP; P05231; 2IL6.
 DR PFAM; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCFMGF.
 DR PROSITE; PR00434; INTERLEUKIN_6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 208
 FT BY SIMILARITY.
 FT INTERLEUKIN-6.
 FT DISULFID 72 78
 FT BY SIMILARITY.
 FT CARBOHYD 38 38
 FT BY SIMILARITY.
 FT CONFLICT 38 38
 FT POTENTIAL.
 SQ SEQUENCE 208 AA; 23758 MW; A0F000B9BA2EC341 CRC64;
 Query Match 54.1%; Score 804; DB 1; Length:208;
 Best Local Similarity 53.3%; Pred. No. 1.90e-148;
 Matches 112; Conservative 48; Mismatches 46; Indels 4; Gaps 2;

Db 1 MNSRFTSAFTPFVAVSLGILLVMTSAFPTGPGLEDGFKNDTPSRLLLTTPKTEALIKRM 60

Search completed: Thu Aug 10 16:28:41 2000
Job time : 38 secs.

```
RT sequence and relation to human interleukin-6.";  
RL Eur. J. Biochem. 176:187-197(1988).  
RN [8]  
RP SEQUENCE OF 66-75; 78-84 AND 128-148.  
RX MEDLINE: 90147691.  
RA Jahnen W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;  
RT "Internal amino acid sequencing of proteins by in situ cyanogen  
RT bromide cleavage in polyacrylamide gels.";  
RL Biochem. Biophys. Res. Commun. 166:139-145(1990).  
RN [9]  
RP SEQUENCE OF 25-45.  
RX MEDLINE: 87092311.  
RA van Snick J., Cayphas S., Vink A., Uyttenhove C., Coulie P.G.,  
RA Rubira M.R., Simpson R.J.;  
RT "Purification and NH2-terminal amino acid sequence of a  
RT T-cell-derived lymphokine with growth factor activity for B-cell  
RT hybridomas.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).  
CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL  
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND  
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN  
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.  
CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL: X06203; CAA29560.1; -  
DR EMBL: M20572; AAA39302.1; -  
DR EMBL: X51457; CAA35824.1; -  
DR EMBL: J03783; AAA39301.1; -  
DR EMBL: X54542; CAA38411.1; -  
DR EMBL: M24221; AAA68814.1; -  
DR PIR: A30531; ICMS6.  
DR HSP: P05231; IALU.  
DR MGD; MGI:96559; IL6.  
DR PFAM: PF00489; IL6.1.  
DR PRINTS; PR00433; IL6GCSFMGF.  
DR PRINTS; PR00434; INTERLEUKIN6.  
DR PROSITE; PS00254; INTERLEUKIN_6; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 211 INTERLEUKIN-6.  
FT DISULFD 70 76 BY SIMILARITY.  
FT DISULFD 99 109 BY SIMILARITY.  
SQ SEQUENCE 211 AA; 24384 MW; BBB47DDA9E86787A CRC64;  
  
Query Match 43.8%; Score 650; DB 1; Length 211;  
Best Local Similarity 41.8%; Pred. No. 1.33e-113;  
Matches 89; Conservative 55; Mismatches 64; Indels 5; Gaps 5;  
  
Db 1 MKFLSARDHPVAF-LGLMLVTTTAPTSQVRGDFED-TTPNR-PVYTTQVQGLITH 57  
QY 1 MNSFSTSAFGPVAFSLGLLLVLPFAFPAP-VPPGEDSKDVAAPHQPLTSSERIDKQIRY 59  
  
Db 58 VLWEIVEMRKELCNGSCNMNDOLAENNLKLPFIQRNDGCGYQGYNQEIICLLKISSGL 117  
QY 60 ILDGISALRKETCKNSKNCCSPSEALAEENNLNPKMAEKDGCFCQSGFNEETCLVKIITGL 119  
  
Db 118 LEYHSYLEYMKNNLKKDKARVLQRTETLIHIFENQEVKDLHKIVLPTPISNALLTDK 177  
QY 120 LEFEVYLEYLNRF-ESSEEQARQVMSKVLQFLQKAKNLDAITTPDTTNASLTK 178  
  
Db 178 LESQEWLRTKTIQIFILKSLEEFKVLTRSTRQ 210  
QY 179 LQAQNWLEDMPHTHLILRSKFEFLQSLRALRQ 211
```

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Run on: Thu Aug 10 16:26:52 2000; MasPar time 13.10 Seconds
Tabular output not generated. 763.396 Million cell updates/sec

Title: >US-09-142-471-5
Description: (1-212) from US09142471.pep
Perfect Score: 1485
Sequence: 1 MNSFSTSAFGVPVAFSLGILL.....LILRSKKEFLQSRRLRQM 212

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir64
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 46.233; Variance 94.667; scale 0.488

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1446	97.4	212	1	interleukin-6 precurs	2.92e-261
2	953	64.2	212	2	prointerleukin 6 - pi	1.35e-160
3	953	64.2	212	2	interleukin 6 - pig	1.35e-160
4	941	63.4	208	2	interleukin-6 precurs	3.60e-158
5	804	54.1	208	1	interleukin-6 precurs	1.39e-130
6	801	53.9	207	2	interleukin 6 - cat	5.54e-130
7	796	53.6	208	1	interleukin-6 - sheep	5.57e-129
8	650	43.8	211	1	interleukin-6 precurs	6.59e-100
9	642	43.2	211	2	interleukin-6 precurs	2.51e-98
10	166	11.2	201	2	myelomonocytic growth	6.08e-10
11	126	8.5	194	2	granulocyte colony-st	5.43e-04
12	119	8.0	656	2	hypothetical protein	4.97e-03
13	113	7.6	214	2	granulocyte colony-st	3.14e-02
14	108	7.3	208	2	granulocyte colony-st	1.40e-01
15	109	7.3	287	2	syntaxin homolog T2H3	1.04e-01
16	109	7.3	321	2	syntaxin homolog T10M	1.04e-01
17	109	7.3	1039	2	myosin heavy chain -	1.04e-01
18	105	7.1	454	2	macrophage scavenger	3.35e-01
19	104	7.0	204	1	granulocyte colony-st	4.47e-01
20	103	6.9	354	2	macrophage scavenger	5.96e-01
21	103	6.9	454	2	macrophage scavenger	5.96e-01
22	101	6.8	314	2	annexin P35 - maize	1.05e+00
23	101	6.8	815	2	high carbon dioxide r	1.05e+00

ALIGNMENTS

RESULT ENTRY	1	24	100	6.7	298	2	S59541	heat shock transcript	1.39e+00
ALTERNATE_NAMES		25	100	6.7	456	2	S62331	phosphotransferase sy	1.39e+00
ORGANISM		26	99	6.7	779	2	JH0102	apolipoprotein B - go	1.84e+00
DATE		27	99	6.7	1392	2	A43336	microtubule-vesicle 1	1.84e+00
ACCESSIONS		28	99	6.7	1392	2	A43336	restin - human	1.84e+00
REFERENCE		29	99	6.7	1642	2	T08880	NMDA receptor-binding	1.84e+00
#authors		30	98	6.6	199	1	B38285	interleukin-11 precu	2.42e+00
#journal		31	98	6.6	241	1	RN218	phosphoprotein p - hu	2.42e+00
#title		32	98	6.6	520	2	S35575	myosin heavy chain, c	2.42e+00
#cross-references		33	97	6.5	341	2	G02515	afaptin 1 - human	3.19e+00
#accession		34	96	6.5	692	2	S54214	flagellar biosynthesi	4.19e+00
#molecule_type		35	97	6.5	880	2	T02245	hypothetical protein	3.19e+00
#residues		36	96	6.5	2767	1	UIHU	hypothetical protein	4.19e+00
##cross-references		37	95	6.4	303	2	S75557	myoglobin precurs	5.49e+00
##note		38	95	6.4	341	2	S40612	myosin-related protei	5.49e+00
		39	95	6.4	533	2	S33744	cyclodiene insectici	5.49e+00
		40	95	6.4	3738	2	T05501	hypothetical protein	5.49e+00
		41	94	6.3	174	2	T10268	granulocyte colony-st	7.18e+00
		42	94	6.3	736	2	C69451	cationic amino acid t	7.18e+00
		43	94	6.3	759	2	JN0435	RNA-directed RNA poly	7.18e+00
		44	94	6.3	1764	2	S37827	hypothetical protein	7.18e+00
		45	94	6.3	4869	2	S66572	ryanodine receptor ty	7.18e+00

IVHUB2 #type complete
Interleukin-6 precursor - human
B-cell differentiation factor; B-cell hybridoma growth factor; B-cell stimulating factor 2 (BSF-2); CTL differentiation factor; IL-6; interferon beta-II-a; megakaryocyte potentiation factor
#formal_name Homo sapiens #common_name man
28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
A32648; A25692; A26966; A33515; A25801; A25921; I52193;
I56003; A27601; B27601; A60400; A29085; A61159; A61462;
A48419; C48419; B48419; JX0305; S04982
A32648
Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimoto, Y.
EMBO J. (1987) 6:2939-2945
Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene.
#cross-references MUID:88082664
#accession A32648
##molecule_type DNA
##residues 1-212 #label YAS
##cross-references GB:Y00081; NID:g29494; PIDN:CAA68278.1; PID:g29495
##note the authors translated the codon CAG for residue 130 as Glu

REFERENCE A91051
Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. (1986) 5:2529-2537
Structure and expression of cDNA and genes for human interferon-beta-2, a distinct species inducible by growth-stimulatory cytokines.
#cross-references MUID:87053818
#accession A25692
##molecule_type mRNA
##residues 1-212 #label ZIL
##cross-references GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674
A93387
Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura, S.I.; Nakajima, K.; Koyama, K.; Iwamatsu, A.; Tsunawasa, S.; Sakiyama, F.; Matsui, H.; Takahara, Y.; Taniguchi, T.; Kishimoto, T.
Nature (1986) 324:73-76
Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocytes to produce immunoglobulin.
#cross-references MUID:87065033
#accession A26966

```

##molecule_type mRNA
##residues 1-212 ##label HIR
##cross-references GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850
REFERENCE
#authors Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
#journal Biochem. Biophys. Res. Commun. (1989) 163:1056-1062
#title Deletion of 3' untranslated region of human BSF-2 mRNA causes
stabilization of the mRNA and high-level expression in
mouse NIH3T3 cells.
#cross-references MUID:89391958
#accession A33515
##molecule_type mRNA
##residues 1-212 ##label TON
##cross-references GB:M29150; NID:g186349; PIDN:AAA59154.1; PID:g307063
REFERENCE
#authors Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.;
Tavernier, J.; Fiers, W.
#journal Eur. J. Biochem. (1986) 159:625-632
#title Structural analysis of the sequence coding for an inducible
26-kDa protein in human fibroblasts.
#cross-references MUID:87004683
#accession A25801
##molecule_type DNA: mRNA
##residues 1-212 ##label HAE
##cross-references GB:X04403
##experimental_source fibroblast
REFERENCE
#authors May, L.T.; Helfgott, D.C.; Sehgal, P.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:8957-8961
#title Anti-beta-Interferon antibodies inhibit the increased
expression of HLA-B7 mRNA in tumor necrosis factor-treated
human fibroblasts: structural studies of the beta-2
interferon involved.
#cross-references MUID:87067433
#accession A25921
##molecule_type mRNA
##residues 1-212 ##label MAY
##cross-references GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
REFERENCE
#authors Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.;
Ogawa, M.
#journal Behring Inst. Mitt. (1988) 83:40-47
#title Interleukin 6: Identification as a hematopoietic
colony-stimulating factor.
#cross-references MUID:89193317
#accession I52193
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-212 ##label WON
##cross-references GB:M54894; NID:g186351; PIDN:AAC41704.1; PID:g186352
REFERENCE
#authors Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.;
Aarden, L.A.
#journal J. Immunol. (1987) 139:4116-4121
#title Molecular cloning and expression of hybridoma growth factor
in Escherichia coli.
#cross-references MUID:88088768
#accession I56003
##status translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-212 ##label BRA
##cross-references GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
REFERENCE
#authors Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De
Ley, M.; Billiau, A.
#journal J. Immunol. (1988) 140:1534-1541
#title Separation and comparison of two monokines with
lymphocyte-activating factor activity: IL-1-beta and
hybridoma growth factor (HGF). Identification of
leukocyte-derived HGF as IL-6.
#cross-references MUID:88154445
#accession A27601
##molecule_type protein

```

```

##residues 28-51,'X','53-57,'X','59,'X',61 ##label VAN1
#accession B27601
##molecule_type protein
##residues 30-56,'XX','59-61,'X',63 ##label VA2
REFERENCE
#authors Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
#journal J. Immunol. (1990) 144:1808-1816
#title The human lung fibroblast cell line, MRC-5, produces multiple
factors involved with megakaryocytopoiesis.
#cross-references MUID:90171574
#accession A60400
##molecule_type protein
##residues 30-43 ##label YAM
REFERENCE
#authors Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.;
Takatsuki, F.; Shimizu, M.; Murashima, A.; Tsunasawa, S.;
Sakiyama, F.; Kishimoto, T.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:228-231
#title Human beta-cell differentiation factor defined by an
anti-peptide antibody and its possible role in autoantibody
production.
#cross-references MUID:87092370
#accession A29085
##molecule_type protein
##residues 29-42 ##label HIR2
REFERENCE
#authors Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.;
Hara, T.; Ishikawa, H.; Arimura, H.; Konno, K.
#journal Anticancer Res. (1991) 11:961-968
#title Purification and characterization of human fibroblast derived
differentiation inducing factor for human monoblastic
leukemia cells identical to interleukin-6.
#cross-references MUID:91290785
#accession A61159
##molecule_type protein
##residues 30-42 ##label NOD
##experimental_source fibroblast
REFERENCE
#authors Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno,
A.
#journal J. Mol. Cell. Immunol. (1989) 4:203-212
#title Interleukin 6 is the principal cytolytic T lymphocyte
differentiation factor for thymocytes in human leukocyte
conditioned medium.
#cross-references MUID:90121567
#accession A61462
##molecule_type protein
##residues 28-48 ##label MIN
##experimental_source leukocyte-conditioned medium
REFERENCE
#authors May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal,
P.B.
#journal Cytokine (1991) 3:204-211
#title Marked cell-type-specific differences in glycosylation of
human interleukin-6.
#cross-references MUID:91355644
#accession A48419
##molecule_type protein
##residues 30-37,'X',39-40 ##label MAY2
##experimental_source FS-4 fibroblasts
##note sequence extracted from NCBI backbone
##note this 28-30K form contained both N-linked and O-linked
carbohydrate; a 25K form containing only N-linked
carbohydrate was also found
#accession C48419
##molecule_type protein
##residues 28-40 ##label MAY3
##experimental_source FS-4 fibroblasts
##note sequence extracted from NCBI backbone (NCBIP:63787)
##note this 23-25K form contained O-linked but not N-linked
carbohydrate
REFERENCE
#authors Orita, T.; Oheda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.;
JX0305

```

QY	181	AQOWLEDMTHILRSIKFQSRSLRALROM	212
RESULT	3	I46590	#type complete
ENTRY		interleukin 6 - pig	
TITLE		#formal_name Sus scrofa domestica	#common_name domestic pig
ORGANISM		21-Feb-1997	#sequence_revision 21-Feb-1997
DATE		16-Jul-1999	#text_change
ACCESSIONS		I46590	

REFERENCE
 #authors Mathialagan, N.; Bixby, J.; Roberts, M.R.
 #journal Mol. Reprod. Dev. (1992) 32:324-330
 #title Expression of interleukin-6 in porcine, ovine, and bovine
 preimplantation conceptuses.
 #cross-references MUID:92360284
 #accession I46590
 ##status preliminary; translated from GB/EMBL/DBJ
 ##molecule_type mRNA
 ##residues 1-212 ##label MAT
 ##cross-references GB:M80259; NID:g164514; PIDN:AAC27127.1; PID:g164515

GENETICS
 #gene IL-6
 #superfamily interleukin-6
 #length 212 #molecular-weight 23952 #checksum 759

CLASSIFICATION
SUMMARY

Query Match 64.2%; Score 953; DB 2; Length 212;
 Best Local Similarity 61.3%; Pred. No. 1.35e-160;
 Matches 130; Conservative 42; Mismatches 40; Indels 0; Gaps 0

QY	1	MNSFSTSAFGVAFSLGGLLVLPAAFPAPVPGEDSKDVAAPHRQPTTSTSERIDKQIRYI	60
Db	61	LGKISARCMCKEYKCEKNSKEYLAENNLNLPKMAEKDGFQSGFNQETCLMRITGLV	120
QY	61	LDGISLRKCTCNKSNWCESSPEALAENNLNLPKMAEKDGFQSGFNEETCLVKIITGLL	120
Db	121	EFQIYLDYQKEYESNKGNYEAVOISFKALITQTLROKGNPKDKATTNPPTNAGLLDKLQ	180
QY	121	EFVYLEYLQNRPFSEBQARAVQMSKVLQYLOKRAKNLDAITTPDPTTNALLTKLQ	180
Db	181	SQNEWMNTKIILRLSLEDFLQFSLRAIRIM	212
QY	181	AONQWLEDMPTHLRLSLKFELOPSLRALROM	212

RESULT	4
ENTRY	T09216
TITLE	interleukin-6 precursor - horse
ORGANISM	#formal_name Equus caballus #common_name domestic horse
DATE	11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
ACCESSIONS	T09216
REFERENCE	Z116613
#authors	Swiderski, C.E.; Horohov, D.W.
#submission	submitted to the EMBL Data Library, July 1996
#accession	T09216

```

##status      preprimary; translated from GB/EMBL/DDBJ
##molecule_type  mRNA
##residues      1-208  ##label SWI
##cross-references  EMBL:U64794; NID:g2654387; PID:g2654388

GENETICS
#gene      IL-6
CLASSIFICATION
#superfamily  interleukin-6
KEYWORDS
#length 208 #molecular-weight 23419 #checksum 3370

Query Match      63.4%; Score 941; DB 2; Length 208;
Best Local Similarity 60.4%; Pred. No. 3.60e-158;
Matches 128; Conservative 46; Mismatches 34; Indels 4; Gaps 3

Db 1 MNSFFTSTVTPVAFSLGLLLVMATFTPTPLPGED--E-TTNSNGLLTTADKTKHIIKYI 57

```

```
||||| 1 MNSFSTSAFGVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
Db 58 LGKISALKNECNFKSCENKEVLAENNLNPKMAEKDCGFCGSGFNOETCLMKITITGLS 117
Qy 61 LDGISALRKETCNKSNCESSPEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLL 120
Db 118 EFQIYLEYLQNEFKGKENIKTMQISIKVLQIILQMKMPE-VTTDPDTAKSKSLAKLH 176
Qy 121 EFQIYLEYLQNEFKGKENIKTMQISIKVLQIILQMKMPE-VTTDPDTAKSKSLAKLH 176
Db 177 SONWLKNTHTLILRSLEDFLQSLRAVRIM 208
Qy 181 AQNWLEDMPTHLILRSLEDFLQSLRAVRIM 212

RESULT 5
ENTRY A56610 #type complete
TITLE Interleukin-6 precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS A56610; S22162
REFERENCE A56610
#authors Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
#journal DNA Seq. (1992) 2:411-413
#title Nucleotide sequence of bovine interleukin-6 cDNA.
#cross-references MUID:93076003
#accession A56610
#status preliminary
#molecule_type mRNA
#residues 1-208 #label DR0
#cross-references EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194
#experimental_source BLV induced B cell-lymphosarcoma
#note sequence extracted from NCBI backbone (NCBIP:118917)
CLASSIFICATION #superfamily interleukin-6
KEYWORDS cytokine
SUMMARY #length 208 #molecular-weight 23758 #checksum 8010

Query Match 54.1%; Score 804; DB 1; Length 208;
Best Local Similarity 53.3%; Pred. No. 1.39e-130;
Matches 112; Conservative 48; Mismatches 46; Indels 4; Gaps 2;

Db 1 MNSRFTSAFTFVSLGILLVMTSAFTPGPLGDEKNDTPGRLLTTPTEKTEALIKRM 60
Qy 1 MNSFSTSAFGVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
Db 61 VDKISAMKEICEKNDCESSKETLAENKLNPKMAEKDCGFCGSGFNOETCLITRTAGLL 120
Qy 61 LDGISALRKETCNKSNCESSPEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLL 120
Db 121 EYQIYLDYLONEGNGENVRDLRKNRTIQLIOLKQIADL--ITTP--ATNTDILLEKMQ 176
Qy 121 EFQIYLEYLQNEFKGKENIKTMQISIKVLQIILQMKMPE-VTTDPDTAKSKSLAKLH 176
Db 177 SNEWVKNKAKIILIRNLFLQSLRAIR 206
Qy 181 AQNWLEDMPTHLILRSLEDFLQSLRAIR 210

RESULT 6
ENTRY I46084 #type complete
TITLE Interleukin 6 - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
ACCESSIONS I46084
REFERENCE I46084
#authors Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
#journal Proc. Soc. Exp. Biol. Med. (1993) 204:301-305
#title Molecular cloning and characterization of a cDNA encoding feline interleukin-6.

||||| 1 MNSFSTSAFGVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
Db 58 LGKISALKNECNFKSCENKEVLAENNLNPKMAEKDCGFCGSGFNOETCLMKITITGLS 117
Qy 61 LDGISALRKETCNKSNCESSPEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLL 120
Db 118 EFQIYLEYLQNEFKGKENIKTMQISIKVLQIILQMKMPE-VTTDPDTAKSKSLAKLH 176
Qy 121 EFQIYLEYLQNEFKGKENIKTMQISIKVLQIILQMKMPE-VTTDPDTAKSKSLAKLH 176
Db 177 SONWLKNTHTLILRSLEDFLQSLRAVRIM 208
Qy 181 AQNWLEDMPTHLILRSLEDFLQSLRAVRIM 212

RESULT 7
ENTRY S29549 #type complete
TITLE Interleukin-6 - sheep
ORGANISM #formal_name Ovis orientalis aries, Ovis ammon aries
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
ACCESSIONS S29549
REFERENCE S29549
#authors Ebrahimi, B.
#submission submitted to the EMBL Data Library, October 1992
#accession S29549
#status preliminary
#molecule_type mRNA
#residues 1-208 #label EBR
#cross-references EMBL:X68723
CLASSIFICATION #superfamily interleukin-6
SUMMARY #length 208 #molecular-weight 23526 #checksum 7927

Query Match 53.6%; Score 796; DB 1; Length 208;
Best Local Similarity 52.9%; Pred. No. 5.57e-129;
Matches 111; Conservative 47; Mismatches 48; Indels 4; Gaps 2;

Db 1 MNSRFTSAFTFVSLGILLVMTSAFTPGPLGDEKNDTPGRLLTTPTEKTEALIKHI 60
Qy 1 MNSFSTSAFGVAFSLGILLVLPAAFPAPVPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
Db 61 VDKISAMKEICEKNDCESSKETLAENKLNPKMAEKDCGFCGSGFNOETCLITRTAGLL 120
Qy 61 LDGISALRKETCNKSNCESSPEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLL 120
Db 121 EYQIYLDYLONEGNGENVRDLRKNRTIQLIOLKQIADL--ITTP--ATHTDILLEKMQ 176
Qy 121 EFQIYLEYLQNEFKGKENIKTMQISIKVLQIILQMKMPE-VTTDPDTAKSKSLAKLH 176
Db 177 SNEWVKNKAKIILIRNLFLQSLRAIR 206
Qy 181 AQNWLEDMPTHLILRSLEDFLQSLRAIR 210

RESULT 8
ENTRY ICMS6 #type complete
TITLE Interleukin-6 precursor - mouse
```


ALTERNATE_NAMES B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte-stimulating factor; IL-6; interferon beta-II; interleukin-HP1; myeloid differentiation inducer MGI-2A; plasmacytoma growth factor

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999

ACCESSIONS A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S10241; S38254

REFERENCE A30531

#authors Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.

#journal J. Immunol. (1988) 141:3875-3881

#title Genomic structure of the murine IL-6 gene. High degree conservation of potential regulatory sequences between mouse and human.

#cross-references MUID:89035525

#accession A30531

#molecule_type DNA

#residues 1-211 #label TAN

#cross-references GB:M20572; NID:g198369; PIDN:AAA39302.1; PID:g387386

REFERENCE A27610

#authors Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Simpson, R.J.

#journal Eur. J. Immunol. (1988) 18:193-197

#title cDNA cloning of murine interleukin-HP1: homology with human interleukin 6.

#cross-references MUID:88166883

#accession A27610

#molecule_type mRNA

#residues 1-211 #label TAN

#cross-references GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702

REFERENCE A30571

#authors Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Clark, S.C.; Wong, G.G.; Rudnikoff, S.

#journal J. Immunol. (1989) 142:1372-1376

#title The murine IL-6 gene maps to the proximal region of chromosome 5.

#cross-references MUID:89124383

#accession A30571

#molecule_type mRNA

#residues 5-211 #label MOC

#cross-references GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699

REFERENCE S01323

#authors Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.

#journal Eur. J. Biochem. (1988) 176:187-197

#title Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and relation to human interleukin-6.

#cross-references MUID:88329059

#accession S01323

#molecule_type protein

#residues 25-166, 'X', 168-211 #label SIM

#note Fig. 10 in having 103-Asn

REFERENCE S12103

#authors Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.

#journal Nucleic Acids Res. (1990) 18:6455

#title Cloning and sequence analysis of the cDNA for murine interleukin-6.

#cross-references MUID:91057159

#accession S12103

#molecule_type mRNA

#residues 1-211 #label GRE

#cross-references EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728

REFERENCE A90157

#authors Jahnke, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.

#journal Biochem. Biophys. Res. Commun. (1990) 166:139-145

#title Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage in polyacrylamide gels.

#cross-references MUID:90147691

#accession E34047

#molecule_type protein

#residues 66-69, 'X', 71-75; 78-94; 128-148 #label JAS

REFERENCE A26662

#authors Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simpson, R.J.

#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:9679-9683

#title Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine with growth factor activity for B-cell hybridomas.

#cross-references MUID:87092311

#accession A26662

#molecule_type protein

#residues 25-39, 'X', 41-42, 'X', 44-45 #label VSN

REFERENCE A40486

#authors Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.

#journal Proc. Natl. Acad. Sci. U.S.A. (1988) 85:7099-7103

#title Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone isolated from bone marrow stromal cells.

#cross-references MUID:89017145

#accession A40486

#molecule_type mRNA

#residues 1-211 #label CHI

#cross-references GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410

REFERENCE A60799

#authors Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; Sachs, L.

#journal Blood (1988) 72:2070-2073

#title The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6.

#cross-references MUID:89062753

#accession A60799

#molecule_type protein

#residues 77-98 #label SHA

REFERENCE S10241

#authors Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.

#journal J. Exp. Med. (1990) 171:965-970

#title DNA rearrangement and constitutive expression of the interleukin 6 gene in a mouse plasmacytoma.

#cross-references MUID:90171860

#accession S10241

#status preliminary

#molecule_type DNA

#residues 1-6 #label BLA

#cross-references EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860

REFERENCE S38254

#authors Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.

#journal Eur. J. Biochem. (1993) 217:53-59

#title Specific covalent modification of the tryptophan residues in murine interleukin-6. Effect on biological activity and conformational stability.

#cross-references MUID:94039075

#accession S38254

#status preliminary

#molecule_type protein

#residues 38-60; 75, 'X', 77-79; 176-203 #label ZHA

GENETICS

#gene IL-6

#map_position 5

#introns 7/1; 68/3; 106/3; 156/3

CLASSIFICATION #superfamily interleukin-6

KEYWORDS Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; macrophage; rheumatoid arthritis

FEATURE

1-24 #domain signal sequence #status predicted #label SIG\

25-211 #product interleukin-6 #status experimental #label MAT

SUMMARY #length 211 #molecular-weight 24384 #checksum 5652

Query Match 43.8%; Score 650; DB 1; Length 211;

Best Local Similarity 41.8%; Pred. No. 6.59e-100;

Matches 89; Conservative 55; Mismatches 64; Indels 5; Gaps 5;

```

Db 1 MKFLSARDHPVAF-LGLMLVTATAPPTSOVRGDFTE-TTPNR-PVYTTSQVGLITH 57
QY 1 MNSFSTSAFGPVAFSLGLLVLPAAFPAP-VPPGEDSKDVAAPHRQPLTSSERIDKQIRY 59

Db 58 VLWEIVEMRKELCNGNSDCMNDALAEENNLKLPFIQRNDGICYGYNOEICLLKISSGL 117
QY 60 ILDGISALRKETCNKSNMCESSPEALAEENNLKPKMAEKDGCFOGFEETCLVKIITGL 119

Db 118 LEVHSYLEYKMNKDKKARVLDQRTETLIHFNQSVKDLHKVLPPTPSNALLTDK 177
QY 120 LEFEVYLEYLNRF-ESSEQARAVQMSTKVLIQLOKAKNLDAITPDPPTNASLLTK 178

Db 178 LESQEWLTKTIQIFILKSLEELFKVTLRSTRQ 210
QY 179 LOAQNWLEDMPHTLILRSKLEFLQSLRALRQ 211

RESULT 9
ENTRY #34247 #type complete
TITLE interleukin-6 precursor - rat
ALTERNATE_NAMES IL-6
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
ACCESSIONS A34247
REFERENCE Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
#journal J. Biol. Chem. (1989) 264:16072-16082
#title Structure of the rat interleukin 6 gene and its expression in macrophage-derived cells.
#cross-references MUID:89380206
#accession A34247
#status preliminary
#molecule_type mRNA
#residues 1-211 ##label NOR
##cross-references GB:M26744; NID:g204915; PIDN:AAA7659.1; PID:g204916
CLASSIFICATION #superfamily interleukin-6
KEYWORDS cytokine; growth factor; immunoregulation; lymphokine; macrophage
SUMMARY #length 211 #molecular-weight 24357 #checksum 5864

Query Match 43.2%; Score 642; DB 2; Length 211;
Best Local Similarity 40.8%; Pred. No. 2.51e-98;
Matches 87; Conservative 60; Mismatches 61; Indels 5; Gaps 5;

Db 1 MKFLSARDHPVAF-LGLMLVTATAPPTSOVRGDFTE-TTPNR-PVYTTSQVGLITY 57
QY 1 MNSFSTSAFGPVAFSLGLLVLPAAFPAP-VPPGEDSKDVAAPHRQPLTSSERIDKQIRY 59

Db 58 VLWEIVEMRKELCNGNSDCMNDALAEENNLKLPFIQRNDGICYGYNOEICLLKISSGL 117
QY 60 ILDGISALRKETCNKSNMCESSPEALAEENNLKPKMAEKDGCFOGFEETCLVKIITGL 119

Db 118 LEFEVYLEYLNRF-ESSEQARAVQMSTKVLIQLOKAKNLDAITPDPPTNASLLTK 178
QY 120 LEFEVYLEYLNRF-ESSEQARAVQMSTKVLIQLOKAKNLDAITPDPPTNASLLTK 178

Db 178 LESQEWLTKTIQIFILKSLEELFKVTLRSTRQ 210
QY 179 LOAQNWLEDMPHTLILRSKLEFLQSLRALRQ 211

RESULT 10
ENTRY #A42247 #type complete
TITLE myelomonocytic growth factor precursor - chicken
ALTERNATE_NAMES colony-stimulating factor cmfG
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
ACCESSIONS A42247; S03633
REFERENCE Sterneck, E.; Blattner, C.; Graf, T.; Leutz, A.

```

```

#journal Mol. Cell. Biol. (1992) 12:1728-1735
#title Structure of the chicken myelomonocytic growth factor gene and specific activation of its promoter in avian myelomonocytic cells by protein kinases.
#cross-references MUID:92195319
#accession A42247
#status preliminary
#molecule_type DNA
#residues 1-201 ##label STE
#note sequence extracted from NCBI backbone (NCBIN:89832, NCBIP:89836)

REFERENCE S03633
Leutz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.; Pan, Y.C.E.; Smart, J.; Hayman, M.; Graf, T.
#journal EMBO J. (1989) 8:175-181
#title Molecular cloning of the chicken myelomonocytic growth factor (cmfG) reveals relationship to interleukin 6 and granulocyte colony stimulating factor.
#cross-references MUID:89231616
#accession S03633
#molecule_type mRNA
#residues 1-201 ##label LEU
##cross-references EMBL:X14477; NID:g63596; PIDN:CAA32639.1; PID:g63597
CLASSIFICATION #superfamily interleukin-6
KEYWORDS glycoprotein
FEATURE
1-23 #domain signal sequence #status predicted #label SIG\
24-201 #product myelomonocytic growth factor #status predicted #label MAT\
123,137 #binding site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 201 #molecular-weight 22373 #checksum 9000

Query Match 11.2%; Score 166; DB 2; Length 201;
Best Local Similarity 22.8%; Pred. No. 6.08e-10;
Matches 45; Conservative 43; Mismatches 103; Indels 6; Gaps 5;

Db 8 LALALVLGAPQQA-LH-CAPLAELSGDHFOLFHLKNE-LFTRKIRGDVAALQAVCDTF 64
QY 16 LGLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKS 75

Db 65 QLCTEELQLVQDPDHLVQ-APLDQCHKRGFAEVCFTQIRAGLHAYHDSIGAVLRLLPN 123
QY 76 NMCESSPEALAEENNLKPKMAEKDGCFOGFEETCLVKIITGLLEFEVYLEYLNRFES 135

Db 124 HTTIVETLQDAANLSNIQQOMEDLGLDVTPLPAEORSPPPTSGFPQ--QQVGGFFIL 181
QY 136 SEEQARAVQMSTKVLIQLOKAKNLDAITPDPPTNASLLTKLQAOQNQWLEDMPTHLIL 195

Db 182 ANFORLETAVALRHL 198
QY 196 RSLKEFLQSLRALRQM 212

RESULT 11
ENTRY #T09255 #type fragment
TITLE granulocyte colony-stimulating factor precursor - cat (fragment)
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
ACCESSIONS T09255
REFERENCE Z16630
Dunham, S.P.; Onions, D.E.
#submission submitted to the EMBL Data Library, September 1996
#description Cloning, sequence and expression of feline granulocyte colony stimulating factor.
#accession T09255
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-194 ##label DUN
##cross-references EMBL:Y08558; NID:e1006755; PID:e270012

```

REFERENCE
S02493
#authors Simpson, R.J.; Nice, E.C.; Nicola, N.A.
#journal Biol. Chem. Hoppe-Sevler (1987) 368:1327-1331
##cross-references GB:M13926; NID:g193451; PIDN:AAA37672.1; PID:g309240

```
#title      Structural studies on the murine granulocyte
            colony-stimulating factor.
#cross-references MUID:88106998
#accession   S02493
##status     preliminary
##molecule_type protein
##residues   31-34,'X',36-43;48-51,'X',53-57,'X',60-71;159-164,'X',
            166-176;183-198,'X',200 #label SIM

GENETICS
#introns     14/1; 71/3; 107/3; 156/3
CLASSIFICATION #superfamily interleukin-6
KEYWORDS       cytokine; growth factor; macrophage; monomer
SUMMARY        #length 208 #molecular-weight 22421 #checksum 6232

Query Match      7.3%; Score 108; DB 2; Length 208;
Best Local Similarity 27.0%; Pred. No. 1.40e-01;
Matches 20; Conservative 17; Mismatches 36; Indels 1; Gaps 1;

Db 56 QVRKIQAGSVLLEQLCATYKLCHEPELVLLGSLGIPK-ASLSGCSQALQQTQCLSQL 114
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 56 QIRYILDGISALRKETCNKSNCESSPEALAEENLNLPKMAEKDGCFCQSGFNEETCLVKI 115
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 115 HSLCLYQGLQAL 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 116 ITGLEFEVYLEYL 129
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
ENTRY   T01430      #type complete
TITLE   syntaxin homolog T2H3.1 - Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear
            cress
DATE    12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
            24-Mar-1999
ACCESSIONS T01430
REFERENCE  Z14324
#authors   Kalicki, J.; Gibson, A.
#submission submitted to the EMBL Data Library, August 1998
#description The sequence of A. thaliana T2H3.
#accession T01430
##status   translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-287 #label KAL
##cross-references EMBL:AF075597; NID:g3298610; PID:g3377798
##experimental_source cultivar Columbia

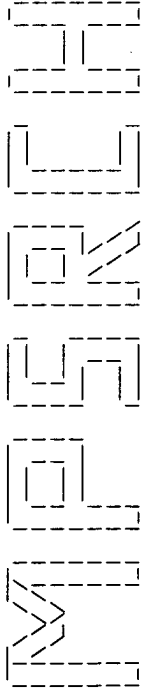
GENETICS
#map_position 4
#introns      64/2; 156/3; 186/3; 211/3; 237/3; 259/3
#note         T2H3.1
SUMMARY       #length 287 #molecular-weight 32420 #checksum 2900

Query Match      7.3%; Score 109; DB 2; Length 287;
Best Local Similarity 23.8%; Pred. No. 1.04e-01;
Matches 20; Conservative 24; Mismatches 37; Indels 3; Gaps 3;

Db 105 LMPFTGDNKGHREVMLETHEITLLRKSEKRLQMLSTGRFSESNLRKNVQSLATDLQ 164
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 129 LQNRFESEEQARAVQSTKVLIQFKAKNLDAITTPDTTNASLLTKIQ-AQNQWLE 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 165 NLSMELR-RKQSTYIKR-LQOQKE 186
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 188 DMPHTLILRLSLEFLQSLRALRQ 211
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: Thu Aug 10 16:27:46 2000
Job time : 54 secs.
```



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 10 16:31:13 2000; MasPar time 5.55 Seconds

Tabular output not generated. 551.323 Million cell updates/sec

Title: >US-09-142-471-5
Description: (1-212) from US09142471.pep
Perfect Score: 1485
Sequence: 1 MNSFSTSAFGPVAFSGLL.....LILRSLEKFLQSLRALROM 212

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 30.636; Variance 159.462; scale 0.192

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description	Pred. No.
1	1446	97.4	212	5	5510472-2	atent No. 5510472	2.90e-106
2	1446	97.4	212	1	US-08-792-	Sequence 9, Applicatio	2.90e-106
3	1264	85.1	185	1	US-08-231-	Sequence 4, Applicatio	2.31e-91
4	1264	85.1	185	1	US-07-918-	Sequence 4, Applicatio	2.31e-91
5	1264	85.1	185	4	PCT-US93-0	Sequence 4, Applicatio	2.31e-91
6	1260	84.8	185	1	US-07-918-	Sequence 8, Applicatio	4.91e-91
7	1260	84.8	185	4	PCT-US93-0	Sequence 8, Applicatio	4.91e-91
8	1260	84.8	185	1	US-08-231-	Sequence 8, Applicatio	4.91e-91
9	1257	84.6	185	1	US-07-632-	Sequence 1, Applicatio	8.64e-91
10	1257	84.6	185	5	5186931-2	atent No. 5186931	8.64e-91
11	1257	84.6	185	1	US-08-231-	Sequence 2, Applicatio	8.64e-91
12	1257	84.6	185	2	US-08-766-	Sequence 5, Applicatio	8.64e-91
13	1257	84.6	185	1	US-07-918-	Sequence 2, Applicatio	8.64e-91
14	1257	84.6	185	1	US-08-246-	Sequence 2, Applicatio	8.64e-91
15	1257	84.6	185	4	PCT-US93-0	Sequence 2, Applicatio	8.64e-91
16	1257	84.6	186	4	PCT-US94-1	Sequence 20, Applicati	8.64e-91
17	1257	84.6	186	4	US-08-165-	Sequence 163, Applicat	8.64e-91
18	1257	84.6	186	1	US-07-745-	Sequence 20, Applicati	8.64e-91
19	1257	84.6	186	1	US-07-745-	Sequence 20, Applicati	8.64e-91
20	1257	84.6	186	1	US-07-632-	Sequence 2, Applicatio	8.64e-91
21	1257	84.6	186	3	US-08-469-	Sequence 163, Applicat	8.64e-91
22	1257	84.6	186	1	US-07-921-	Sequence 20, Applicati	8.64e-91
23	1257	84.6	187	1	US-07-632-	Sequence 3, Applicatio	8.64e-91

24	1257	84.6	317	4	PCT-US95-0	Sequence 145, Applicat	8.64e-91
25	1257	84.6	317	3	US-08-469-	Sequence 145, Applicat	8.64e-91
26	1253	84.4	184	2	US-08-567-	Sequence 2, Applicatio	1.83e-90
27	1253	84.4	184	1	US-08-567-	Sequence 2, Applicatio	1.83e-90
28	1253	84.4	184	5	5186931-1	atent No. 5186931	1.83e-90
29	1253	84.4	185	1	US-08-231-	Sequence 6, Applicatio	1.83e-90
30	1253	84.4	185	1	US-07-918-	Sequence 6, Applicatio	1.83e-90
31	1253	84.4	185	4	PCT-US93-0	Sequence 6, Applicatio	1.83e-90
32	1253	84.4	185	1	US-08-716-	Sequence 7, Applicatio	1.83e-90
33	1246	83.9	184	2	US-09-008-	Sequence 2, Applicatio	6.85e-90
34	1246	83.9	184	2	US-08-693-	Sequence 2, Applicatio	6.85e-90
35	1245	83.8	183	1	US-08-009-	Sequence 1, Applicatio	8.27e-90
36	1235	83.2	319	4	PCT-US94-0	Sequence 2, Applicatio	5.43e-89
37	1229	82.8	185	4	PCT-US92-0	Sequence 2, Applicatio	1.68e-88
38	1229	82.8	186	1	US-08-209-	Sequence 2, Applicatio	1.68e-88
39	1206	81.2	184	2	US-08-945-	Sequence 8, Applicatio	1.27e-86
40	1204	81.1	184	2	US-08-945-	Sequence 11, Applicati	1.83e-86
41	1196	80.5	184	2	US-08-945-	Sequence 9, Applicatio	8.33e-86
42	1190	80.1	200	1	US-08-209-	Sequence 8, Applicatio	2.58e-85
43	1190	80.1	201	4	PCT-US92-0	Sequence 8, Applicatio	2.58e-85
44	1181	79.5	186	4	PCT-US92-0	Sequence 6, Applicatio	1.40e-84
45	1181	79.5	186	1	US-08-209-	Sequence 6, Applicatio	1.40e-84

ALIGNMENTS

RESULT 1	STANDARD;	PRT;	212 AA.
ID 5510472-2			
XX	xxxxxx		
AC			
XX			
DT			
XX			
DE	Patent No. 5510472		
XX			
CC	Patent No. 5510472		
CC	APPLICANT: REVEL, MICHEL;TIOUAI, PIERRE		
CC	TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN		
CC	INTERFERON-BETA2		
CC	NUMBER OF SEQUENCES: 9		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/07/883,633		
CC	FILING DATE: 15-MAY-1992		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: 208,925		
CC	FILING DATE: 20-NOV-1980		
CC	APPLICATION NUMBER: 449,447		
CC	FILING DATE: 12-DEC-1989		
CC	APPLICATION NUMBER: 860,883		
CC	FILING DATE: 08-MAY-1986		
CC	APPLICATION NUMBER: 208,925		
CC	FILING DATE: 20-NOV-1980		
CC	SEQ ID NO:2		
CC	LENGTH: 212		
CC	SEQUENCE 212 AA; 23718 MW; 222128 CN;		

Query Match 97.4%; Score 1446; DB 5; Length 212;
Best Local Similarity 97.6%; Pred. No. 2.90e-106;
Matches 207; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db	1	MNSFSTSAFGPVAFSGLLLVLPAPVP	PPGDSKDVAAPHROP	LTSSERIDQIRYI	60
Qy	1	MNSFSTSAFGPVAFSGLLLVLPAPVP	PPGDSKDVAAPHROP	LTSSERIDQIRYI	60
Db	61	LDGISALRKETCNKNCMESSKEALAEN	NLNP	KMAEKDCGFCQSGFNEETCLVKITGLL	120
Qy	61	LDGISALRKETCNKNCMESSKEALAEN	NLNP	KMAEKDCGFCQSGFNEETCLVKITGLL	120
Db	121	EFVYLEYLNQNFESSEQARAVQSTKVLI	QFLOKAKNLDAITTPD	TTNASLTKIQ	180
Qy	121	EFVYLEYLNQNFESSEQARAVQSTKVLI	QFLOKAKNLDAITTPD	TTNASLTKIQ	180
Db	181	AQNQLQDWTTHILRSKFQSLRALROM			212

CC ZIP: 10014
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/231,575
CC FILING DATE: 22-APR-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/918,181
CC FILING DATE: 23-JUL-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Sheets, Eric J.
CC REGISTRATION NUMBER: 30,326
CC REFERENCE/DOCKET NUMBER: FOW-2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212-645-1405
CC TELEFAX: 212-645-2054
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 185 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 185 AA; 20965 MW; 169089 CN;
SQ
Query Match 84.8%; Score 1260; DB 1; Length 185;
Best Local Similarity 97.3%; Pred. No. 4,91e-91;
Matches 180; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 1 APVPPGDSKDVAAHPRQPLTSSERIDKQIRYILDGIGSALRKETCNKNMCESSKEALAE 60
QY 28 APVPPGDSKDVAAHPRQPLTSSERIDKQIRYILDGIGSALRKETCNKNMCESSPEALAE 87
Db 61 NNILNPKMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVOMST 120
QY 88 NNILNPKMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVOMST 147
Db 121 KVLQFLQKAKNLDATTPDPTTNASLTKLQAOQNWLDMTTHILRLSKFEFQSSLR 180
QY 148 KVLQFLQKAKNLDATTPDPTTNASLTKLQAOQNWLDMTTHILRLSKFEFLQSLR 207
Db 181 ALRQM 185
QY 208 ALRQM 212
RESULT 9
ID US-07-632-070B-1 STANDARD; PRT; 185 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 1, Application US/07632070B
XX Sequence 1, Application US/07632070B
CC Patent No. 5264209
CC GENERAL INFORMATION:
CC APPLICANT: Mikayama, Toshihumi
CC APPLICANT: APPLICANT: Kadoya, Toshihiko
CC APPLICANT: APPLICANT: Kakitani, Makoto
CC APPLICANT: APPLICANT: Inoue, Hideo
CC TITLE OF INVENTION: Modified hIL-6
CC NUMBER OF SEQUENCES: 3
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Marshall, O'Toole, Gerstein,
CC ADDRESSEE: Murray & Bicknell
CC STREET: 20 South Clark Street, Suite 2100
CC CITY: Chicago
CC STATE: Illinois

CC COUNTRY: United States of America
CC ZIP: 60603
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
CC COMPUTER: IBM COMPATIBLE
CC OPERATING SYSTEM: MS-DOS
CC SOFTWARE: NBI
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/632,070B
CC FILING DATE: 19901221
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: JP 2-32273
CC FILING DATE: 13 FEB 1990
CC APPLICATION NUMBER: JP 2-222353
CC FILING DATE: 22 AUG 90
CC APPLICATION NUMBER: JP 2-250460
CC FILING DATE: 21 SEPT 1990
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 185
CC TYPE: AMINO ACID
CC STRANDEDNESS:
CC TOPOLOGY: Linear
CC SEQUENCE 185 AA; 20981 MW; 169252 CN;
SQ
Query Match 84.6%; Score 1257; DB 1; Length 185;
Best Local Similarity 97.3%; Pred. No. 8,64e-91;
Matches 180; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 1 APVPPGDSKDVAAHPRQPLTSSERIDKQIRYILDGIGSALRKETCNKNMCESSKEALAE 60
QY 28 APVPPGDSKDVAAHPRQPLTSSERIDKQIRYILDGIGSALRKETCNKNMCESSPEALAE 87
Db 61 NNILNPKMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVOMST 120
QY 88 NNILNPKMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYLQNRFPESSEQARAVOMST 147
Db 121 KVLQFLQKAKNLDATTPDPTTNASLTKLQAOQNWLDMTTHILRLSKFEFQSSLR 180
QY 148 KVLQFLQKAKNLDATTPDPTTNASLTKLQAOQNWLDMTTHILRLSKFEFLQSLR 207
Db 181 ALRQM 185
QY 208 ALRQM 212
RESULT 10
ID 5186931-2 STANDARD; PRT; 185 AA.
XX
AC xxxxxx
XX
DT
XX
DE Patent No. 5186931
XX Patent No. 5186931
CC APPLICANT: Kishimoto, Tadamitsu; Hirano, Toshio; Akiyama, Yukio;
CC Okano, Akira; Matsui, Hiroshi; Takahara, Yoshiyuki
CC TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
CC MARROW TRANSPLANTATION
CC NUMBER OF SEQUENCES: 2
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/366,866
CC FILING DATE: 15-JUN-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 81,746
CC FILING DATE: 05-AUG-1987
CC SEQ ID NO: 2:
CC LENGTH: 185
CC SEQUENCE 185 AA; 20981 MW; 169252 CN;
SQ
Query Match 84.6%; Score 1257; DB 5; Length 185;

W A S E R E H (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 10 16:25:48 2000; MasPar time 8.44 Seconds
Tabular output not generated. 594.691 Million cell updates/sec

Title: >US-09-142-471-5
Description: (1-212) from US09142471.pap
Perfect Score: 1485
Sequence: 1 MNSFSTSAFGVPVAFSLGILL.....LILSLKEFLQRSRLALRQ M 212

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseq

Statistics: Mean 32.908; Variance 163.071; scale 0.202

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	1485	100.0	212	1	W35878 Human interleukin-6 (I	3.46e-114
2	1485	100.0	212	1	W33843 Human interleukin-6 (I	3.46e-114
3	1446	97.4	212	1	R49249 Sequence of human B-ce	7.79e-111
4	1446	97.4	212	1	P80269 Recombinant interleuki	7.79e-111
5	1446	97.4	212	1	P90047 pBSF2-L8 sequence	7.79e-111
6	1446	97.4	212	1	P70238 Interferon-beta 2a.	7.79e-111
7	1446	97.4	212	1	P90436 Interferon-beta-2.	7.79e-111
8	1446	97.4	212	1	P90469 Interleukin-6	7.79e-111
9	1446	97.4	212	1	R72317 Interferon-beta2A.	7.79e-111
10	1446	97.4	212	1	R33430 IFN-beta-2a.	7.79e-111
11	1446	97.4	212	1	R05415 Human B-cell different	7.79e-111
12	1446	97.4	212	1	R49041 Human interleukin-6.	7.79e-111
13	1446	97.4	212	1	R34726 Human IL-6 (for modifi	7.79e-111
14	1446	97.4	212	1	P90371 pBSF2-L8	7.79e-111
15	1443	97.2	212	1	P81156 Human B-cell different	1.41e-110
16	1441	97.0	212	1	P82577 Leader sequence of	2.10e-110
17	1441	97.0	212	1	P81176 Sequence of the BSP-2	2.10e-110
18	1441	97.0	212	1	P90121 Human lymphocyte recep	2.10e-110
19	1437	96.8	212	1	R33384 Cytokine hIL-6.	4.62e-110
20	1421	95.7	212	1	R12521 B cell differentiation	1.10e-108
21	1410	94.9	211	1	R25279 Mutant human BCDF.	9.66e-108
22	1280	86.2	188	1	W95011 Human interleukin-6 (I	1.39e-96
23	1273	85.7	208	1	P81160 Polypeptide with B-cell	5.53e-96

ALIGNMENTS

RESULT 1

ID	W35878	standard; protein; 212 AA.	
AC	W35878		
DT	27-APR-1998	(first entry)	
DE	Human interleukin-6 (IL-6)	mutein polypeptide.	
KW	Interleukin-6; IL-6; mutein; antagonist; human; mutation; treatment;		
KW	plasmocytoma; myeloma; osteoporosis; autoimmune disease.		
OS	Synthetic.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..28	
FT		/note= "signal peptide"	
FT	Protein	29..212	
FT		/note= "mature protein"	
FT	Misc_difference 82	/label= K82P	
FT		/note= "wild type Lys is replaced by Pro"	
FT	Misc_difference 187	/label= Q187E	
FT		/note= "wild type Gln is replaced by Glu"	
FT	Misc_difference 190	/label= T190P	
FT		/note= "wild type Thr is replaced by Pro"	
FT	Misc_difference 198	/label= F198L	
FT		/note= "wild type Phe is replaced by Leu"	
FT	Misc_difference 204	/label= S204R	
FT		/note= "wild type Ser is replaced by Arg"	
PN	WO9738103-A1.		
PD	16-OCT-1997.		
PF	09-APR-1996; E01506.		
PR	09-APR-1996; WO-E01506.		
PI	(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.		
PI	Ehlers M, Grotzinger J, Rose-John S;		
DR	WPI: 97-512720/47.		
PT	New interleukin-6 mutein polypeptides - useful as IL-6 antagonists		
PT	for treating e.g. plasmocytoma/myeloma, osteoporosis and neoplastic		
PT	and autoimmune diseases.		
PS	Claim 1; Pages 15-16; 38pp; English.		
CC	This is a interleukin-6 (IL-6) mutein polypeptide. This IL-6 mutein		
CC	comprises a mature protein of 184 amino acids. This polypeptide is		
CC	created by point mutations on the wild-type human IL-6, at positions		
CC	54, 159, 162, 170,176 of the mature human IL-6. The DNA sequence encoding		
CC	this IL-6 mutein and the sequences encoding variants having the same		
CC	activity resulting from the degeneracy of the genetic code or point		
CC	mutations can be used to transform a host cell. The IL-6 mutein can act		

Sequence of variant of 1.81e-95
Chimeric sIL-6R/IL-6 p 1.81e-95
Full length interleuki 3.26e-95
Interleukin-6 receptor 3.98e-95
Full length interleuki 7.19e-95
Polypeptide with B-cel 1.30e-94
Segment of human B cel 1.30e-94
Ala-BCDF. 1.30e-94
Full length interleuki 1.30e-94
Human interleukin-6. 1.30e-94
Recombinant interleuki 1.30e-94
hIL-6 protein. 1.30e-94
Interleukin-6. 2.86e-94
Interleukin-6. 2.86e-94
Polypeptide with human 2.86e-94
Interleukin 6. smulator 2.86e-94
Human B-cell smulator 2.86e-94
Synthetic interleukin- 2.86e-94
Human interleukin-6 fr 2.86e-94
Full length interleuki 2.86e-94
Human fusion polypepti 2.86e-94
Human fusion polypepti 2.86e-94

as IL-6 antagonist. This polypeptide and its fragments can be used for treating diseases in which IL-6 has a pathogenic action such as plasmacytoma myeloma, osteoporosis and neoplastic and autoimmune diseases. 212 AA;

Query Match 100.0%; Score 1485; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.46e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
QY 1 MNSFSTSAFGVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60

Db 61 LDGTSALRKETCNKSNMCSSPEALAEENLNLPMKAEKDCGFCQSGFNEETCLVKIITGLL 120
QY 61 LDGTSALRKETCNKSNMCSSPEALAEENLNLPMKAEKDCGFCQSGFNEETCLVKIITGLL 120

Db 121 EFEVYLEYLNQRFESSEQARAVOMSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
QY 121 EFEVYLEYLNQRFESSEQARAVOMSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180

Db 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212
QY 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212

RESULT 2
ID W33643 standard; protein; 212 AA.
AC W33643;
DT 27-APR-1998 (first entry)
DE Human interleukin-6 (IL-6) mutein polypeptide.
KW Interleukin-6; IL-6; mutein; antagonist; human; mutation; treatment; plasmacytoma; myeloma; osteoporosis; autoimmune disease.
OS Synthetic.
FS Key Location/Qualifiers
FH Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..212
FT /note= "mature protein"
FT Misc_difference 82
FT /label= K82P
FT /note= "wild type Lys is replaced by Pro"
FT Misc_difference 187
FT /label= Q187E
FT /note= "wild type Gln is replaced by Glu"
FT Misc_difference 190
FT /label= T190P
FT /note= "wild type Thr is replaced by Pro"
FT Misc_difference 198
FT /label= F198L
FT /note= "wild type Phe is replaced by Leu"
FT Misc_difference 204
FT /label= S204R
FT /note= "wild type Ser is replaced by Arg"
FT W09738104-A1.
FT 16-OCT-1997.
FT 08-APR-1997; E01736.
FT 09-APR-1996; W0-E01506.
FT (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
FT Ehlers M, Grotzinger J, Rose-John S;
FT WPI; 97-512721/47.
FT New interleukin-6 mutein polypeptide - useful as IL-6 antagonist for treating e.g. plasmacytoma/myeloma, osteoporosis and neoplastic and autoimmune diseases
FT Claim 1; Pages 15-16; 37pp; English.
PS This is a interleukin-6 (IL-6) mutein polypeptide. This IL-6 mutein comprises a mature protein of 184 amino acids. This polypeptide is created by point mutations on the wild-type human IL-6, at positions 54, 159, 162, 170, 176 of the mature human IL-6. The DNA sequence encoding this IL-6 mutein and the sequences encoding variants having the same activity resulting from the degeneracy of the genetic code or point

mutations can be used to transform a host cell. The IL-6 mutein can act as IL-6 antagonist. This polypeptide and its fragments can be used for treating diseases in which IL-6 has a pathogenic action such as plasmacytoma myeloma, osteoporosis and neoplastic and autoimmune diseases. 212 AA;

Query Match 100.0%; Score 1485; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.46e-114;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
QY 1 MNSFSTSAFGVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60

Db 61 LDGTSALRKETCNKSNMCSSPEALAEENLNLPMKAEKDCGFCQSGFNEETCLVKIITGLL 120
QY 61 LDGTSALRKETCNKSNMCSSPEALAEENLNLPMKAEKDCGFCQSGFNEETCLVKIITGLL 120

Db 121 EFEVYLEYLNQRFESSEQARAVOMSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180
QY 121 EFEVYLEYLNQRFESSEQARAVOMSTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQ 180

Db 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212
QY 181 AQNWLEDMPTHLILRSKEFLQSLRALROM 212

RESULT 3
ID R49249 standard; Protein; 212 AA.
AC R49249;
DT 15-SEP-1994 (first entry)
DE Sequence of human B-cell differentiation factor (BCDF) encoded by cDNA.
DE cDNA.
KW B-cell differentiation factor; BCDF; antitumour; antiviral; lymphokine.
OS Homo sapiens.
PN EP-585957-A-
PD 09-MAR-1994.
PF 06-AUG-1987; 111409.
PR 06-AUG-1986; JP-184858.
PR 27-AUG-1986; JP-200433.
PR 18-DEC-1986; JP-302699.
PR 13-MAY-1987; JP-116332.
PA (AJIN) AJINOMOTO KK.
PA (KISH) KISHIMOTO T.
PI Akiyama Y, Hirano T, Kishimoto T, Matsui H, Okano A;
PI Takahara Y;
DR WPI; 94-076278/10.
DR N-PSDB; Q56265.
PT New non-glycosylated human B-cell differentiation factor - lacking signal sequence and produced in bacteria, useful as immuno therapeutic for stimulating antibody prodn, treating cancer etc, also DNA encoding it
PS Claim 2; Fig 5; 63pp; English.
CC Human T cells transformed by human T cell leukaemia virus (HTLV)
CC produce BCDF which has an activity of 5x10(6) units/ml or more. For its prep., RNA is extracted from human T cell line VT-1 (IFO 50096) and used to construct a cDNA library. Oligos are constructed from known N-terminal sequence of BCDF and used to screen the library.
CC One positive clone, contg. plasmid bpsr2-38, was selected and sequenced; it includes the codons for an additional 28 AA N-terminal CC region. A polypeptide corresp. to AAs 28-212 of R49249, and a CC recombinant DNA comprising a gene encoding it are claimed.
SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
QY 1 MNSFSTSAFGVAFSLGLLLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60

Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLNLPKMAEKDGCFCGSGFNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNLPKMAEKDGCFCGSGFNEETCLVKIITGLL 120
 Db 121 EFEVYLEYLQNRRESSEEQARAVOMSTKVLIQFLOKAKNLDAITTPDPTTNASLLTKLQ 180
 QY 121 EFEVYLEYLQNRRESSEEQARAVOMSTKVLIQFLOKAKNLDAITTPDPTTNASLLTKLQ 180
 Db 181 AQNWQLDMTTHILRSKFELQSSLRALROM 212
 QY 181 AQNWQLDMTTHILRSKFELQSSLRALROM 212

RESULT 4
 ID P80269 standard; protein; 212 AA.
 AC P80269;
 DT 08-OCT-1990 (first entry)
 DE Recombinant interleukin 6.
 KW IL-6; interleukin; cancer.
 FH Key Location/Qualifiers
 FT peptide 1..27
 FT /label=signal peptide
 FT modified_site 73..75
 FT /label=Glycosylation site
 FT /note="N-linked"
 FT modified_site 172..174
 FT /label=Glycosylation site
 FT /note="N-linked"
 W08000206-A.
 PN 14-JAN-1988.
 PD 07-JUL-1987; U01611.
 PR 08-JUL-1986; US-883207,
 PA (GENE-) Genetics Inst Inc.
 PI Clark SC, Wong GG, Schendel P, McCoy J;
 DR N-PSDB; N80299.
 DT Prod'n. of non-glycosylated IL-6 - for use in treatment of deficiency disorders in haematopoietic cells and in cancer therapy.
 PS Disclosure; p; English.
 CC The sequence is encoded by DNA carried by PCSF309 in E.coli MC1061 (ATCC 6715) as an EcoRI insert. This can be excised and used to construct an expression plasmid for prod'n. of IL-6. Bacterially produced IL-6 is non-glycosylated. It can be used against diseases caused by decreased levels of either myeloid or lymphoid cells of the haematopoietic system. It may also be used in conjunction with other interleukin therapies or as a hybridoma growth factor in culture medium.
 CC See also P80270.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFLGLLLVLPAAFPAPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYI 60
 QY 1 MNSFSTSAFGPVAFLGLLLVLPAAFPAPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLNLPKMAEKDGCFCGSGFNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNLPKMAEKDGCFCGSGFNEETCLVKIITGLL 120
 Db 121 EFEVYLEYLQNRRESSEEQARAVOMSTKVLIQFLOKAKNLDAITTPDPTTNASLLTKLQ 180
 QY 121 EFEVYLEYLQNRRESSEEQARAVOMSTKVLIQFLOKAKNLDAITTPDPTTNASLLTKLQ 180
 Db 181 AQNWQLDMTTHILRSKFELQSSLRALROM 212
 QY 181 AQNWQLDMTTHILRSKFELQSSLRALROM 212

RESULT 5
 ID - P90047 standard; protein; 212 AA.

P90047;
 DT 1-NOV-1989 (first entry)
 DE pBSF2-L8 sequence
 KW pBSF2-L8; pGEM4; clone; Fc epsilon R-gene; IgE; allergy; peptide.
 PN EP-321842-A.
 PD 28-JUN-1989.
 PR 14-DEC-1988; 120878.
 PR 22-DEC-1987; EP-100814.
 PA (OSAU) Osaka University.
 PI Kishimoto T, Suemura M, Kikutani H, Barsumian EL, Schneider F-J, Schwendenwein R, Sommergruber W, Swetly P;
 DR WPI; 89-186249/26.
 DR N-PSDB; N90131, N90132.
 DT Cloned gene for eukaryotic expression of Fc epsilon receptor
 PT - for use in treatment and prophylaxis of allergy, esp. asthma.
 PS Disclosure; fig 3; 25pp; English.
 CC The sequence is of pBSF2-L8 including the BSF-2 signal
 CC sequence.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFLGLLLVLPAAFPAPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYI 60
 QY 1 MNSFSTSAFGPVAFLGLLLVLPAAFPAPVPPGSDSKDVAAPHRQPLTSSERIDKQIRYI 60
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLNLPKMAEKDGCFCGSGFNEETCLVKIITGLL 120
 QY 61 LDGIALRKETCNKSNMCESSPEALAEANNLNLPKMAEKDGCFCGSGFNEETCLVKIITGLL 120
 Db 121 EFEVYLEYLQNRRESSEEQARAVOMSTKVLIQFLOKAKNLDAITTPDPTTNASLLTKLQ 180
 QY 121 EFEVYLEYLQNRRESSEEQARAVOMSTKVLIQFLOKAKNLDAITTPDPTTNASLLTKLQ 180
 Db 181 AQNWQLDMTTHILRSKFELQSSLRALROM 212
 QY 181 AQNWQLDMTTHILRSKFELQSSLRALROM 212

RESULT 6

ID P70238 standard; protein; 212 AA.
 AC P70238;
 DT 21-MAR-1980 (first entry)
 DE Interferon-beta 2a.
 KW Interferon-beta 2a; therapy.
 OS Homo sapiens.
 PN EP-220574-A.
 PD 06-MAY-1987.
 PF 10-OCT-1986; 114049.
 PR 14-OCT-1985; IL-076714.
 PR 08-MAY-1986; US-860883.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Revel M, Zilberstein A;
 DR WPI; 87-124210/18.
 DR N-PSDB; N70348.
 DT Recombinant human interferon-beta(2A) and beta(2B) - useful for
 PT inflammation, acute phase response or regulation of cell
 PT proliferation
 PS Disclosure; Fig. 1; 17pp; English.
 CC The protein has interferon activity. It inhibits viral replication and
 CC cytopathic effect and induces the proteins typical of the biological
 CC response of human cells to interferon. It is useful for influencing
 CC cell growth and differentiation, esp. during terminal differentiation of
 CC tumour cells and for inhibiting fibroblast proliferation and to prevent
 CC sclerosis after infection. The protein is also useful in the fields of
 CC inflammation acute-phase response or regulation of cell proliferation.
 CC Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 |||||
 QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 |||||
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 |||||
 QY 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 |||||
 Db 121 EFVYLEYLQNRFFESSEEQARAVQSTKVLQFLOKKAENLDAITTPDPTTNASLLTKLQ 180
 |||||
 QY 121 EFVYLEYLQNRFFESSEEQARAVQSTKVLQFLOKKAENLDAITTPDPTTNASLLTKLQ 180
 |||||
 Db 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 |||||
 QY 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 |||||

RESULT 7

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 DT 20-OCT-1989 (first entry)
 DE Interferon-beta-2.
 KW Interferon-beta 2; monoclonal antibodies; human;
 KW acute myelogenous leukaemia; breast cancer; bacterial and
 KW parasitic diseases; bone marrow transplants.
 OS Homo sapiens (human)
 FH EP-326120-A.
 PN 02-AUG-1989.
 PF 25-JAN-1989; 101295.
 PR 26-JAN-1988; IL-088376.
 PA (YEDA) Yeda Research and Dev Co Ltd.
 PI Revel M; Rubinstein M; Moriy Y; Chen L; Novick D; Michalewicz R.
 DR WPI: 89-222084/31.
 DR N-PSDB: N90377.
 PT Monoclonal antibody to human interferon-beta-2
 PT - produced by hybridoma cell line and useful for leukaemia
 PT treatment etc.
 PS Disclosure: fig 1; 26 pp; English.
 CS Interferon-beta-2 (see N90377). Used to make
 CC monoclonal antibodies, and in the treatment of the diseases
 CC in KW above.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 |||||
 QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 |||||
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 |||||
 QY 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 |||||
 Db 121 EFVYLEYLQNRFFESSEEQARAVQSTKVLQFLOKKAENLDAITTPDPTTNASLLTKLQ 180
 |||||
 QY 121 EFVYLEYLQNRFFESSEEQARAVQSTKVLQFLOKKAENLDAITTPDPTTNASLLTKLQ 180
 |||||
 Db 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 |||||
 QY 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 |||||

RESULT 8

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 DT 1-NOV-1989 (first entry)
 DE Interleukin-6
 KW Interleukin-6; lysine-depleted variant;
 KW site-directed mutagenesis; human.

OS Homo sapiens
 PN WO905924-A.
 PD 29-JUN-1989.
 PF 22-DEC-1988; U04633.
 PR 23-DEC-1987; US-137043.
 PA (GENE) Genetics Inst Inc.
 PI Shaw G;
 DR WPI: 89-206594/28.
 DR N-PSDB: N90255.
 PT New lysine depleted variants of polypeptide
 PT - opt. modified with hydrophilic residues,
 PT biologically active but with altered solubility, stability etc.
 PS Disclosure: fig 3; 35pp; English.
 CC DNA of interleukin-6 (see corresp. N90255). Used in the patent
 CC to create lysine depleted variants by site-directed mutagenesis,
 CC or synthesis.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 |||||
 QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 |||||
 Db 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 |||||
 QY 61 LDGIALRKETCNKSNMCESSKEALAEANNLPLKMAEKDGCFCQSGFNEETCLVKIITGLL 120
 |||||
 Db 121 EFVYLEYLQNRFFESSEEQARAVQSTKVLQFLOKKAENLDAITTPDPTTNASLLTKLQ 180
 |||||
 QY 121 EFVYLEYLQNRFFESSEEQARAVQSTKVLQFLOKKAENLDAITTPDPTTNASLLTKLQ 180
 |||||
 Db 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 |||||
 QY 181 AQONQLDMPTHLILRSKFQSSLRALQRM 212
 |||||

RESULT 9

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 ID R72317 standard; Protein; 212 AA.
 AC R72317;
 DT 14-NOV-1995 (first entry)
 DE Interferon-beta2A.
 KW biologically active; interferon-beta2A; IFN-beta2A; cell growth;
 KW terminal differentiation; cancer; inhibit fibroblast proliferation.
 OS Homo sapiens.
 PN EP-645452-A.
 PD 29-MAR-1995.
 PF 10-OCT-1986; 114478.
 PR 14-OCT-1985; IL-076714.
 PR 08-MAY-1986; US-860883.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Revel M, Zilberstein A;
 DR WPI: 95-124593/17.
 DR N-PSDB: Q86523.
 PT A DNA sequence encoding active interferon beta2A - used in the
 PT prodn. of the protein for the treatment of cancer, by inhibition
 PT of fibroblast proliferation
 PS Claim 1; Fig 1; 17pp; English.
 CC Biologically active interferon-beta2A (IFN-beta2A), including the
 CC N-terminus of the mature protein, may be used to influence cell growth
 CC and differentiation esp. terminal differentiation of cancer cells and
 CC to inhibit fibroblast proliferation preventing sclerosis after
 CC infection.
 SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
 Best Local Similarity 97.6%; Pred. No. 7.79e-111;
 Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYI 60
 |||||

QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYI 60

Db 61 LDGISALRKETCNKSNWCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

QY 61 LDGISALRKETCNKSNWCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFESESEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

QY 121 EFVYLEYLQNRFESESEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

Db 181 AQNWQDMTTHILRSFKEFLQSSLRALQRM 212

QY 181 AQNWQDMTTHILRSFKEFLQSSLRALQRM 212

RESULT 10

ID R33430 standard; Protein; 212 AA.

AC R33430;

DT 28-JUL-1993 (first entry)

DE IFN-beta-2a.

KW Interferon; IFN; pharmaceutical; inflammation; acute phase response;

KW regulation; cell; proliferation; inhibition; fibroblast; sclerosis;

KW infection; antiviral; antitumor; human; IFN-beta-1; IFN-beta-2;

KW IFN-beta-2a; IFN-beta-2b.

OS Homo sapiens.

PN EP-536520-A.

PD 14-APR-1993.

PF 10-OCT-1986; 114478.

PR 14-OCT-1985; IL-076714.

PR 08-MAY-1986; US-860883.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Revel M, Zilberstein A;

DR WPI: 93-118821/15.

DR N-PSDB: Q39582.

PT New compsn. contg. human interferon-beta 2A - for treating

PT inflammation and acute phase response, regulating cell

PT proliferation, etc.

PS Disclosure; Fig 1; 16pp; English.

CC This sequence represents interferon (IFN)-beta-2a. This protein was

CC used in the construction of a pharmaceutical composition which was

CC used for treating inflammation, acute phase response, regulation of

CC cell proliferation, inhibition of fibroblast proliferation and for

CC prevention of sclerosis after infection. IFNs are important antiviral

CC and antitumor proteins produced by the human body. The major species

CC of IFN produced by human fibroblasts is IFN-beta-1. This is immuno-

CC logically distinct from IFN-beta-2. Two genes have been found to

CC encode IFN-beta-2, IFN-beta-2a and IFN-beta-2b.

CC Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;

Best Local Similarity 97.6%; Pred. No. 7.79e-111;

Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYI 60

QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYI 60

Db 61 LDGISALRKETCNKSNWCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

QY 61 LDGISALRKETCNKSNWCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFESESEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

QY 121 EFVYLEYLQNRFESESEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

Db 181 AQNWQDMTTHILRSFKEFLQSSLRALQRM 212

QY 181 AQNWQDMTTHILRSFKEFLQSSLRALQRM 212

RESULT 11

ID R05415 standard; protein; 212 AA.

AC R05415;

DT 27-JUL-1990 (first entry)

DE Human B-cell differentiation factor gene product.

KW BSF-2; dhfr; dihydrofolic acid reductase; differentiation.

OS Homo sapiens.

PN J02009388-A.

PD 12-JAN-1990.

PF 8-JUL-1988; 170142.

PR 9-MAR-1988; JP-055270.

PA (AJIN) Ajinomoto KK.

DR WPI: 90-055348/08.

DR N-PSDB: Q01763.

PT Physiologically active protein prepn. -

PT by transforming plasmid having gene coding physiologically

PT active protein and gene of dihydrofolic acid reductase to hamster

PT ovary etc.

PS Example 3; Fig 6; 12pp; Japanese.

CC Gene may be expressed by transforming a dhfr negative strain of CHO cells

CC with an active BSF-2 gene and dhfr carrying vector. BSF-2 gene product

CC is a B-cell differentiating factor.

CC Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;

Best Local Similarity 97.6%; Pred. No. 7.79e-111;

Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYI 60

QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAAPHRQPLTSSERIDKQIRYI 60

Db 61 LDGISALRKETCNKSNWCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

QY 61 LDGISALRKETCNKSNWCSSKEALAEENLNLPKMAEKDGCFCFSGFNEETCLVKIITGLL 120

Db 121 EFVYLEYLQNRFESESEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

QY 121 EFVYLEYLQNRFESESEQARAVOMSTKVLIQFLQKAKNLDATITPDPPTNASLTKLQ 180

Db 181 AQNWQDMTTHILRSFKEFLQSSLRALQRM 212

QY 181 AQNWQDMTTHILRSFKEFLQSSLRALQRM 212

RESULT 12

ID R49041 standard; protein; 212 AA.

AC R49041;

DT 06-SEP-1994 (first entry)

DE Human interleukin-6.

KW Interleukin 6; IL-6; thrombocytopoiesis; surgery; chemotherapy;

KW radiation therapy; bone marrow transplantation; cancer therapy;

KW neoplasia; anti-neoplastic activity.

OS Homo sapiens.

PN W09403492-A.

PD 17-FEB-1994.

PF 01-JUL-1993; A00324.

PR 06-AUG-1992; AU-003983.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (UYME) UNIV MELBOURNE.

PI Simpson RJ, Williams NT;

DR WPI: 94-065607/08.

DR N-PSDB: Q55973.

PT New interleukin-6 variants - capable of stimulating

PT thrombocytopoiesis while exhibiting low hybridoma growth factor

PT activity

PS Disclosure; Page 33; 46pp; English.

CC This sequence is human interleukin-6 (IL-6). IL-6 variants in

CC the form of non-full length molecules can stimulate, enhance or

CC facilitate thrombocytopoiesis without the side effects of other IL-6

CC activities. The IL-6 variants are useful for inducing

CC thrombocytopoiesis in thrombocytopenic patients following surgery.

CC chemotherapy, radiation therapy or bone marrow transplantation. The

CC IL-6 variants may also be useful in cancer therapy where the

CC fragments express anti-neoplastic activity.

CC Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||
QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||

Db 61 LDGIALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||
QY 61 LDGIALRKETCNKSNMCSSPEALAEENLNLPKMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||

Db 121 EFVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQ 180
|||||
QY 121 EFVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQ 180
|||||

Db 181 AQONWLODMPTHLILRSKFQLOSLRALROM 212
|||||
QY 181 AQONWLODMPTHLILRSKFQLOSLRALROM 212
|||||

RESULT 13
ID R34726 standard; protein; 212 AA.
AC R34726;
DT 24-AUG-1993 (first entry)
DE Human IL-6 (for modification).
KW Interleukin-6; stability; blood; cytokine; BSF-2.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..29
FT protein /label= sig_pep
FT /label= mat_protein
PN J05086099-A.
PD 06-APR-1993.
PF 31-JUL-1991; 191475.
PR 31-JUL-1990; JP-204440.
PA (TORA) TORAY IND INC.
DR WPI; 93-149232/18.
PT Modified interleukin-6 derivs. - used to treat platelet-reducing
PT conditions, thrombocytopenia
PS Claim 1; Page 2; 6pp; Japanese.
CC A modified interleukin-6 (IL-6) contg. at least 3 sequences of Asn-X-
CC Thr or Asn-X-Ser, where X is an amino acid other than Pro, is
CC claimed (no specific sequences, nor the sequence below are given
CC in the specification 1).
CC The modified IL-6 can be expected to have higher stability in
CC blood, higher medical effect and higher absorption in the
CC objective organ.
SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||
QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||

Db 61 LDGIALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||
QY 61 LDGIALRKETCNKSNMCSSPEALAEENLNLPKMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||

Db 121 EFVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQ 180
|||||
QY 121 EFVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQ 180
|||||

Db 181 AQONWLODMPTHLILRSKFQLOSLRALROM 212
|||||
QY 181 AQONWLODMPTHLILRSKFQLOSLRALROM 212
|||||

RESULT 14
ID P90371 standard; protein; 212 AA.
AC P90371;
DT 1-NOV-1989 (first entry)
DE pBSF2-L8
KW FC epsilon receptor; cloned gene; IgE; pBSF2-L8; allergy;
KW asthma; BSF-2.
PN EP-321601-A.
PD 28-JUN-1989.
PF 22-DEC-1987; 119080.
PR 22-DEC-1987; EP-119080.
PA (OSAU) Osaka University.
PI Kishimoto T, Suemura M, Kikutani H, Barsumian E;
DR WPI; 89-186101/26.
DR N-PSDB; N90134, N90135, N90136.
PT Cloned genes coding for soluble IgE receptor - comprising modified coding
PT sequence of Fc epsilon receptor gene.
PS Disclosure; fig 3; 19pp; English.
CC Peptide sequence of pBSF2-L8. See also N90134-6.
SQ Sequence 212 AA;

Query Match 97.4%; Score 1446; DB 1; Length 212;
Best Local Similarity 97.6%; Pred. No. 7.79e-111;
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||
QY 1 MNSFSTSAFGPVAFSLGILLVLPAAFPAPVPPGDSKDVAAPHQPLTSSERIDKQIRYI 60
|||||

Db 61 LDGIALRKETCNKSNMCSSKEALAEENLNLPKMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||
QY 61 LDGIALRKETCNKSNMCSSPEALAEENLNLPKMAEKDGCQFSGFNEETCLVKIITGLL 120
|||||

Db 121 EFVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQ 180
|||||
QY 121 EFVYLEYLNRFESSEEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQ 180
|||||

Db 181 AQONWLODMPTHLILRSKFQLOSLRALROM 212
|||||
QY 181 AQONWLODMPTHLILRSKFQLOSLRALROM 212
|||||

RESULT 15
ID P81156 standard; protein; 212 AA.
AC P81156;
DT 10-MAR-1993 (revised)
DT 15-OCT-1990 (first entry)
DE Human B-cell differentiation factor (BCDF).
KW B-cell differentiation factor; BCDF; cancer; autoimmune.
OS Homo sapiens.
PN EP-257406-A.
PD 2-MAR-1988.
PF 6-AUG-1988; 111409.
PR 06-AUG-1986; JP-184858.
PR 27-AUG-1986; JP-200433.
PR 18-DEC-1986; JP-302699.
PR 13-MAY-1987; JP-116332.
PA (AJIN) Ajinomoto KK.
PI Kishimoto TN, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
DR WPI; 88-057698/09.
DR N-PSDB; N81460.
PT Purified polypeptide with B-cell differentiation factor activity -
PT useful in prodn. of antibodies for diagnosis and therapy of
PT cancers, infectious diseases etc.
PS Claim 24; Fig 5; 72pp; English.
CC BCDF may be used in the production and repair of B-cells, it is
CC useful in treatment of autoimmune diseases, malignant tumors and
CC may be used to influence B-cells to produce Abs in vitro.
SQ Sequence 212 AA;

Query Match 97.2%; Score 1443; DB 1; Length 212;
Best Local Similarity 97.2%; Pred. No. 1.41e-110;
Matches 206; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Thu Aug 10 17:13:58 2000

US-09-142-471-5.rag

Page 7

Db 1 MNSTSAFGVVAASLIGLLVLPAPAPAPVPQGDSDVAAPHROPILTSSERIDKQIRY 60
QY 1 MNSTSASFQVAASLIGLLVLPAPAPAPVPQGDSDVAAPHROPILTSSERIDKQIRY 60
Db 61 LDGTSALAKEFCNKSNNMCSSKEALAEENNINLTPMAEKDCQFQSGFNEFCIVKITYGL 120
QY 61 LDGTSALAKEFCNKSNNMCSSKEALAEENNINLTPMAEKDCQFQSGFNEFCIVKITYGL 120
Db 121 EFEPYVLEIQNRFFSSSEQOAPAVOMSTKVLIQIQAKAKMLDAITTPDPPTNASLTKIQ 180
QY 121 EFEPYVLEIQNRFFSSSEQOAPAVOMSTKVLIQIQAKAKMLDAITTPDPPTNASLTKIQ 180
Db 181 AONOMLODMTHLILRSRKEPFIQSSALPROM 212
QY 181 AONOMLEDMPTHILIRSLKEPFIQSSALPROM 212

Search completed: Thu Aug 10 16:26:34 2000
Job time : 46 secs.

This Page Blank (uspto)